

1/36

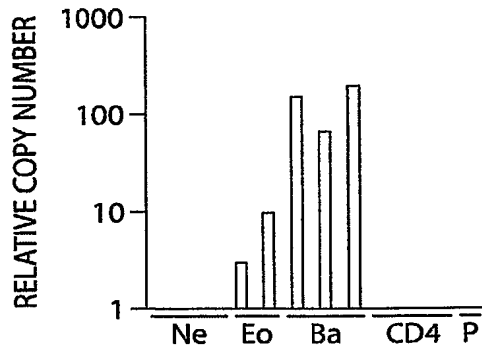


Fig. 1A

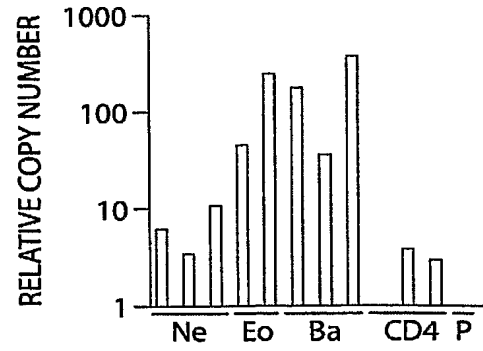


Fig. 1B

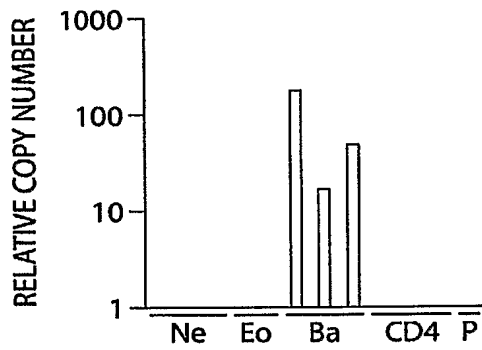


Fig. 1C

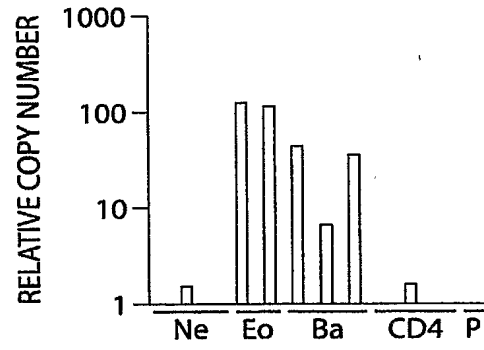


Fig. 1D

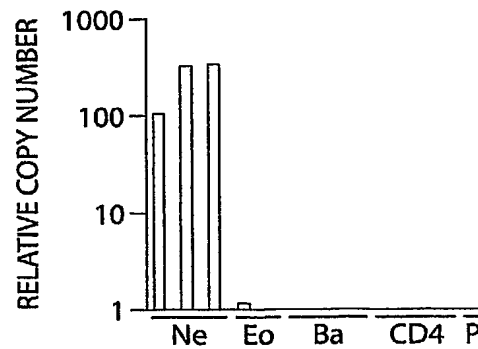


Fig. 1E

2/36

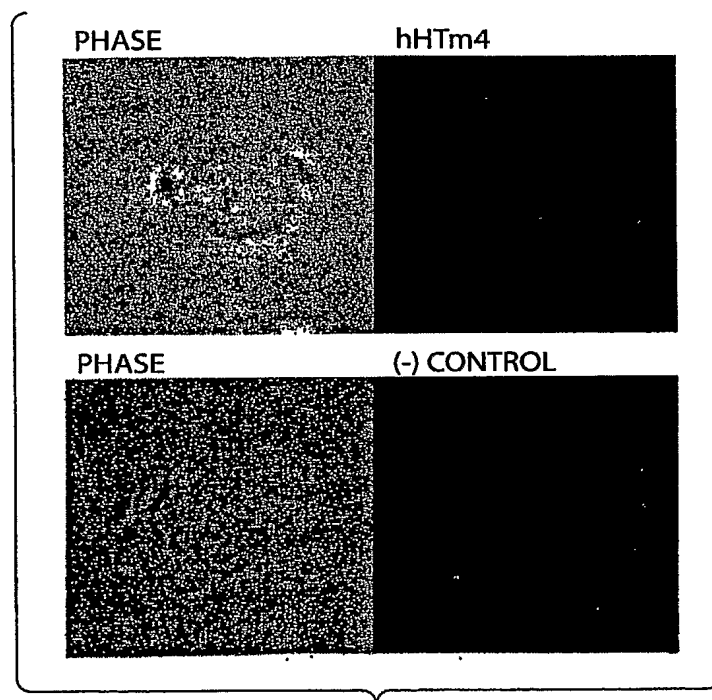


Fig. 2

3/36

Figure 3. Granulocyte subtype-specific transcripts for ion channels and receptors

<u>Ion Channels</u> <u>Transcript (Accession #, GenBank)</u>	<u>Cell-</u> <u>type^a</u>	<u>MC</u>	<u>Ba</u>	<u>Eo</u>	<u>Ne</u>	<u>PI</u>	<u>CD4</u>	<u>CD8</u>	<u>CD14</u>	<u>CD19</u>	<u>Fb</u>	<u>TC^b</u>	<u>Gene Functions</u>
<u>Ca²⁺ channel type A1 D (BE550599)</u> <u>aquaporin 9 (NM_020980) 602914</u>	Ba, Eo Ne	0.1 0.7	1.7 0.1	1.5 0.4	0.4 137.4	0.0 0.4	0.3 0.9	0.1 0.1	0.0 8.6	0.3 0.1	0.0 0.2	0 7	facilitates uptake of the metalloids arsenite and antimonite
<u>K⁺ channel Kir 1.3 (U73191) 600359</u>	Ne	0.9	0.2	0.4	99.5	0.7	0.2	0.0	0.8	0.0	0.0	5	Andersen syndrome (170390) and Bartter syndrome (241200)
<u>K⁺ channel Kir 2.1 (AF153820) 600681</u>	Ne	0.7	3.8	5.3	40.7	0.4	0.2	0.5	1.5	0.7	1.1	6	Andersen syndrome (170390) and Bartter syndrome (241200)
<u>GPCR</u> <u>histamine H₄ R (AF312230) 606792</u>	Ba	0.7	34.2	9.4	0.7	0.4	0.8	0.5	0.6	0.0	0.1	0	expression of HRH4 conferred sensitivity
<u>PGE₂ R type 3a2 (X83858) 176806</u> <u>C3a R (U62027) 605246</u> <u>CCR3 (NM_001837) 601268</u>	Ba Ba, Eo Ba, Eo	0.8 11.8 0.6	10.3 55.7 117.4	0.1 39.4 90.9	0.7 2.0 24.9	0.6 1.6 0.2	0.3 1.6 0.5	0.2 1.5 0.4	0.2 3.0 0.2	0.5 0.6 0.2	1.7 0.5 0.4	0 3 0	signaling pathways anaphylatoxin receptor importance for eosinophil responses
<u>CRTH2 (NM_004778) 604837</u>	Ba, Eo	1.1	26.0	38.2	2.0	0.8	1.4	1.0	1.2	0.9	0.5	0	mediate signals to the interior of the cell via activation of heterotrimeric G proteins
<u>EMR-1 (NM_001974) 600493</u>	Ba, Eo	0.8	33.5	90.9	4.2	3.4	1.7	0.8	7.1	1.6	0.5	1	Probably involved in cellular response to a hormone
<u>adenosine A₃ R (NM_000677) 600445</u> <u>P2Y2 purinergic R (NM_002564) 600041</u>	Eo Eo	2.6 0.1	2.9 0.1	15.4 5.5	2.3 0.1	1.2 0.2	1.6 0.1	0.5 0.3	2.0 1.2	0.5 0.2	0.5 0.1	0 0	cardioprotective function P2RY2 may participate in control of the cell cycle of endometrial carcinoma cells
<u>GPR 105 purinergic R (NM_014879)</u>	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	2	GPR105 is a G-protein-coupled receptor identifying a quiescent, primitive population of hematopoietic cells restricted to bone marrow; GPR105 might play an important role in peripheral and neuroimmune function
<u>GPR, Edg-4 (AF011466) 605110</u>	Eo, Ne	1.3	2.8	15.9	24.2	0.1	3.6	5.0	3.8	1.9	0.9	2	edg-4 mrna was expressed in mouse islets; edg-4 (lpa2) r is a distinctive functional marker for ovarian carcinoma, and is expressed both as the wild-type and a carboxyl-terminally extended gain-of-function mutant.
<u>PAR1-like GPR43 (NM_005306)</u>	Eo, Ne	0.3	0.7	12.4	35.2	0.8	0.1	0.1	0.7	0.4	0.1	0	the highest levels of gpr43 were

Fig. 3A

603823														found in immune cells: gpr43 is highly restricted in hematopoietic tissues
C5a R (NM_001736) 113995	Ne	2.3	21.6	13.6	92.6	2.3	1.2	0.5	25.6	1.0	0.4	5		receptor for the chemotactic and inflammatory peptide anaphylatoxin c5a. this receptor stimulates chemotaxis, granule enzyme release and superoxide anion production.
CXCR1 IL-8R (NM_000634) 146929	Ne	0.2	4.3	0.3	83.4	0.4	0.3	0.2	0.2	0.1	0.1	0		receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to mgsa (gro) with a low affinity.
CXCR2 IL-8R (NM_001557)	Ne	0.2	1.1	1.5	112.1	2.7	0.3	0.8	0.7	0.6	0.0	1		receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to gro/mgsa and nap-2 also with a high affinity.
formyl peptide R 1 (NM_002029) 136537	Ne	2.8	23.5	8.8	282.9	3.6	1.3	0.7	62.6	1.1	0.5	0		HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED

Fig. 3B

Fig. 3B

5/36

Fig. 3C

formyl peptide R 2 (<u>U81501</u>)	Ne	0.4	0.5	0.6	75.5	0.1	1.0	0.6	6.0	0.8	0.1	5	VIA A G-PROTEIN THAT ACTIVATES PHOSPHATIDYLINOSITOL- CALCIUM SECOND MESSENGER SYSTEM. likely FPR2, mediates superoxide production at high concentrations of fMLF. CSL2 is an anaphylatoxin- binding protein with unique ligand binding and signaling properties GPR86 proved to be a G(i)- coupled receptor displaying a high affinity for ADP, similar to the P2Y(12) receptor and can therefore be tentatively called P2Y(13) PAR2 plays a key role in chronic joint inflammation
	Ne	0.1	0.9	0.8	3.4	0.0	0.3	0.2	1.0	0.1	0.3	2	
	Ne	0.3	0.2	17.9	88.2	1.9	0.1	0.2	12.3	0.6	0.0	1	
	Ne	0.1	0.3	2.2	36.2	0.1	0.7	0.1	1.6	0.4	1.2	15	
	Ba	19.4	219.0	4.6	5.5	1.4	5.1	0.8	1.4	0.4	0.2	0	
Other Receptors Fcε RI α (<u>BC005912</u>) <u>147138</u> <u>HTm4</u> (<u>L35848</u>) <u>606498</u> IL-3 R (<u>NM_002183</u>) <u>308385</u> CD244 NK cell R <u>NM_016382</u> <u>605554</u> fibroblast growth factor R 2 (<u>NM_022969</u>) <u>176943</u> IL-5R α (<u>M75914</u>) <u>147851</u> Siglec 8 (<u>NM_014442</u>) <u>605639</u>	Ba	0.6	133.1	6.9	3.5	0.2	0.5	0.4	0.1	0.2	0.0	1	responsible for initiating the allergic response Cell cycle regulator promotes the proliferation and differentiation of hematopoietic cells engagement of 2B4 with specific antibody activates NK cytolytic activity Receptor for acidic and basic fibroblast growth factors. lacking either 115ra or Sox4 have defects in B-cell development SIGLEC8 expression on eosinophils but not other leukocytes Signaling from the KIT receptor tyrosine kinase is essential for primordial germ cell growth both in vivo and in vitro OBPP1 is almost exclusively expressed on B cells. MS4A2 Allergic disease receptor-mediated endocytosis
	Ba	0.6	52.6	2.0	0.7	0.2	0.3	0.2	0.7	0.1	0.1	0	
	Ba, Eo	0.3	56.0	16.5	1.2	0.1	0.4	3.5	5.2	1.1	0.1	0	
	Ba, Eo	0.1	27.9	12.1	0.2	0.1	0.1	0.2	0.1	0.1	1.0	17	
	Ba, Eo	0.9	20.5	30.4	0.6	0.1	0.1	0.1	0.1	0.2	0.1	0	
CD117 c-KIT (<u>NM_000222</u>) <u>164920</u> SigtecB D86358 <u>604405</u> Fcε RIβ (<u>NM_000139</u>) <u>147138</u> low density lipoprotein R	Eo	1.8	0.3	17.4	0.4	0.3	0.2	0.1	0.2	0.5	0.2	0	responsible for initiating the allergic response Cell cycle regulator promotes the proliferation and differentiation of hematopoietic cells engagement of 2B4 with specific antibody activates NK cytolytic activity Receptor for acidic and basic fibroblast growth factors. lacking either 115ra or Sox4 have defects in B-cell development SIGLEC8 expression on eosinophils but not other leukocytes Signaling from the KIT receptor tyrosine kinase is essential for primordial germ cell growth both in vivo and in vitro OBPP1 is almost exclusively expressed on B cells. MS4A2 Allergic disease receptor-mediated endocytosis
	MC	89.0	7.2	4.2	1.2	0.8	0.2	0.5	0.1	0.1	0.5	15	
	MC	5.6	0.2	0.0	0.2	0.5	0.0	0.0	0.0	0.4	0.0	0	
	MC, Ba	22.3	44.3	0.4	0.6	1.6	0.5	0.2	0.0	0.3	0.1	0	
	MC, Ba	20.7	20.4	1.3	1.8	2.3	2.1	3.4	3.5	0.8	6.3	34	

6/36

<u>(NM_000527) 606945</u> <u>TRK neurotrophin R (NM_002529)</u> <u>191315</u>	MC, Ba	4.6	7.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0	participates in the primary signal transduction mechanism of NGF; is also an immunoregulatory cytokine acting on monocytes
butyrophilin like R (AK025267).	Ne	1.1	1.7	1.5	6.9	1.5	1.7	1.6	0.9	1.5	1.3	1	1	his gene is mainly expressed in small intestine, colon, testis, and leukocytes
<u>CD120a, TNF-R-1 (NM_001065)</u> <u>191190</u>	Ne	1.7	1.2	7.8	74.7	1.3	2.2	5.9	17.4	0.6	16	35	35	<u>Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Contributes to the induction of noncytotoxic TNF effects including anti-viral state and activation of the acid sphingomyelinase.</u>
<u>CD95, Fas, APO-1 (AA164751) 134637</u>	Ne	1.4	10.9	7.3	50.4	1.3	5.6	4.8	3.6	2.6	9.7	7	7	<u>Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted</u>

Fig. 3D

[illegible]

a. Cell-type specificity was obtained by comparing the "normalized AD" levels of each gene in mast cells (MC; average of 2 experiments), basophils (Ba; average of 3 experiments), eosinophils (Eo; average of 4 experiments), neutrophils (Ne; average of 4 experiments), platelets (Pl), CD4⁺ cells (CD4), CD8⁺ cells (CD8), CD14⁺ cells (CD14), CD19⁺ cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb).

Fig. 3E

8/36

	CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
Spink5	21	17	11	22	16	30	15	28	36	129	104
chymase human	1221	47	65	45	12	101	62	108	59	104	45
tryptase alpha	21179	212	40	33	25	184	139	104	17	52	39
tryptase beta	25414	195	113	49	28	152	10	122	113	93	6
tryptase delta	349	45	6	23	55	74	113	11	10	42	11
tryptase gamma	654	56	19	38	78	28	24	81	230	142	83
TRPV2	129	37	15	97	99	259	137	133	67	97	110
ANKTM1_	28	28	8	38	30	96	18	14	46	11	28
Cannabinoid receptor type 1	50	41	14	47	36	27	61	41	56	18	54
Cannabinoid receptor type 2	160	369	226	578	177	271	530	324	232	212	421

Fig. 4A

9/36

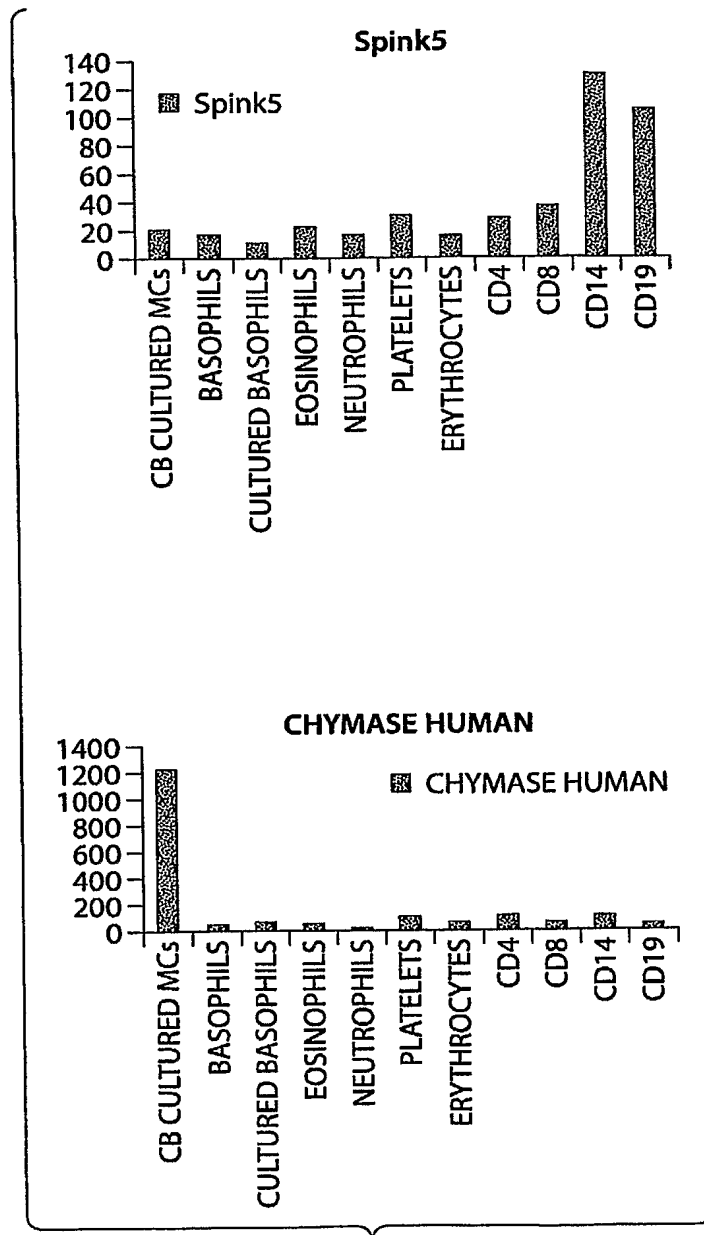


Fig. 4B

10/36

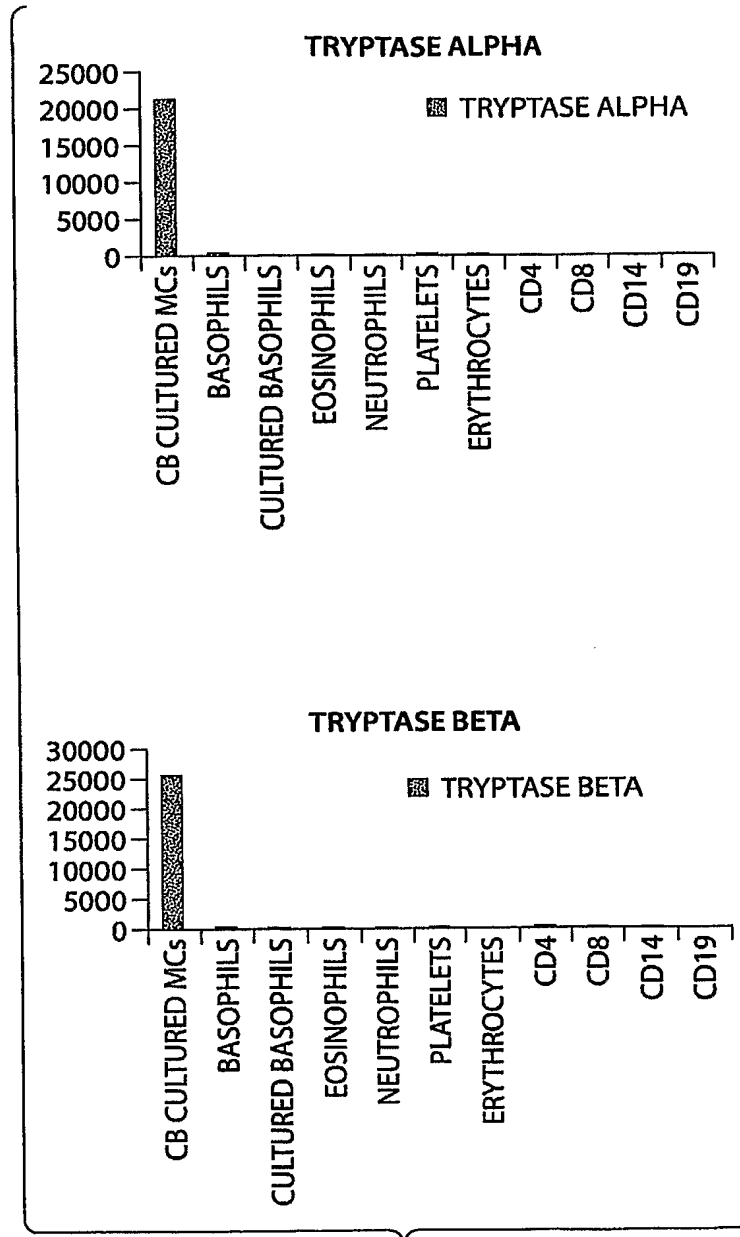


Fig. 4C

11/36

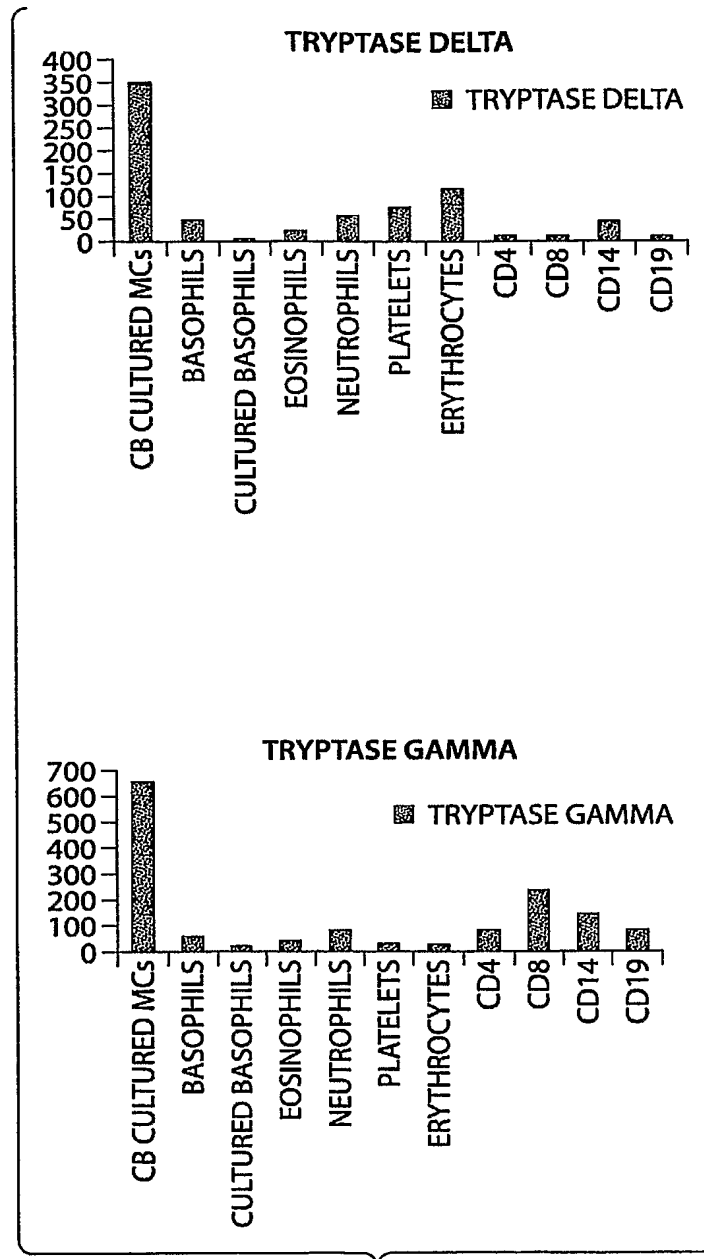


Fig. 4D

12/36

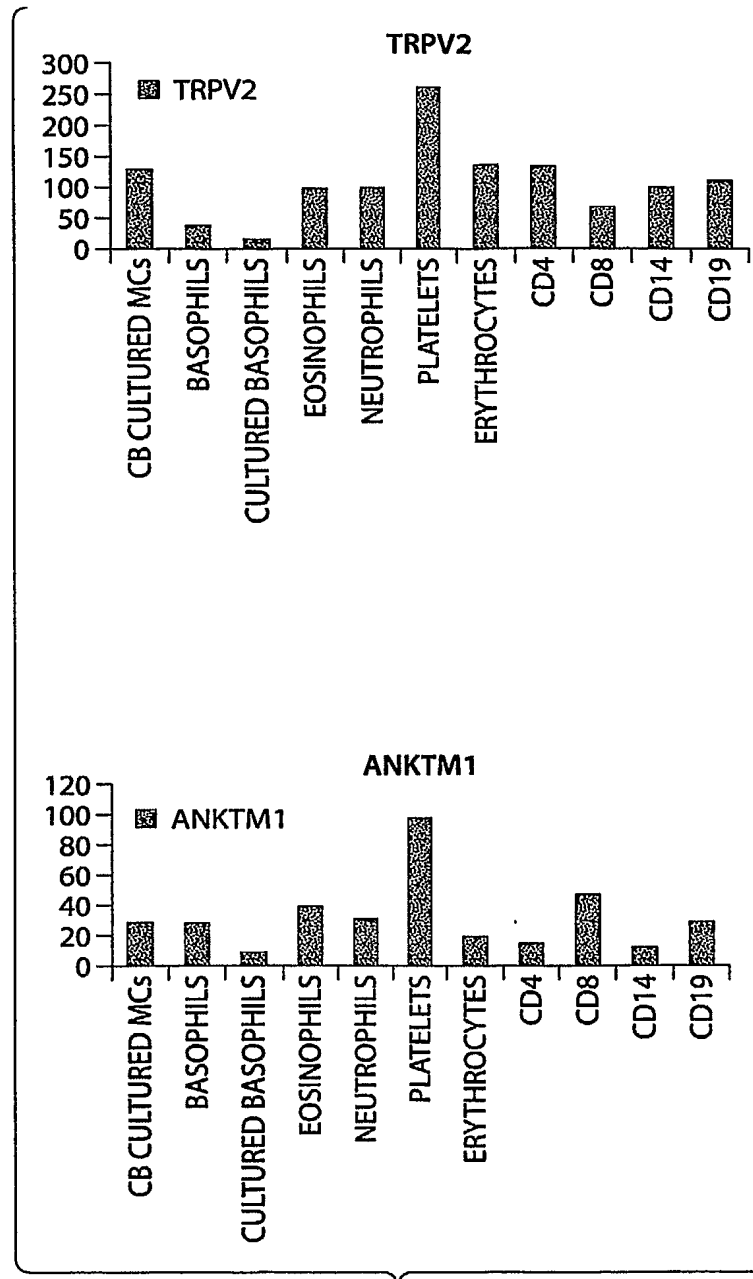


Fig. 4E

13/36

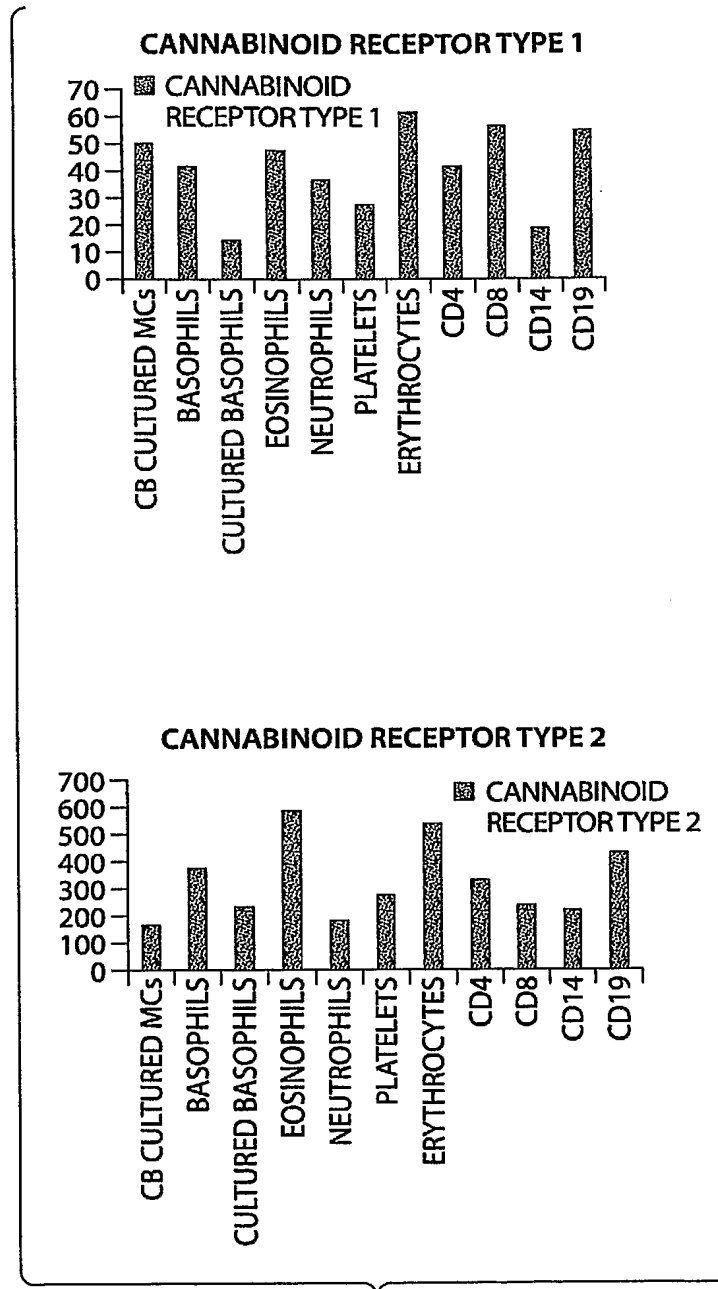


Fig. 4F

14/36

CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
86	28	39	26	37	125	46	103	95	85	28
4	45	1004	59	84	18	68	31	68	451	13
165	84	51	258	1261	31	42	13	18	1105	125
375	780	227	1755	4237	199	375	286	58	2963	214
49	614	384	461	3269	146	318	8	9	1247	52
28	50	45	154	389	120	148	127	35	539	86
7	58	34	18	23	13	106	14	286	68	204
22	17	21	27	28	35	11	28	110	88	111
30	54	134	66	61	149	95	39	247	147	271
35	138	81	88	93	191	132	57	257	21	267
24	31	23	21	21	53	27	33	135	19	173
139	140	85	157	144	280	210	35	239	152	196
11	45	41	50	41	88	15	19	72	77	85
41	43	31	20	52	31	121	96	163	26	193
27	83	24	41	49	61	239	92	323	56	72
68	89	41	51	95	75	97	76	169	36	196
144	621	83	1334	2386	107	146	145	52	2154	99
18	14	5	28	37	86	12	13	14	32	23

Fig. 5A

15/36

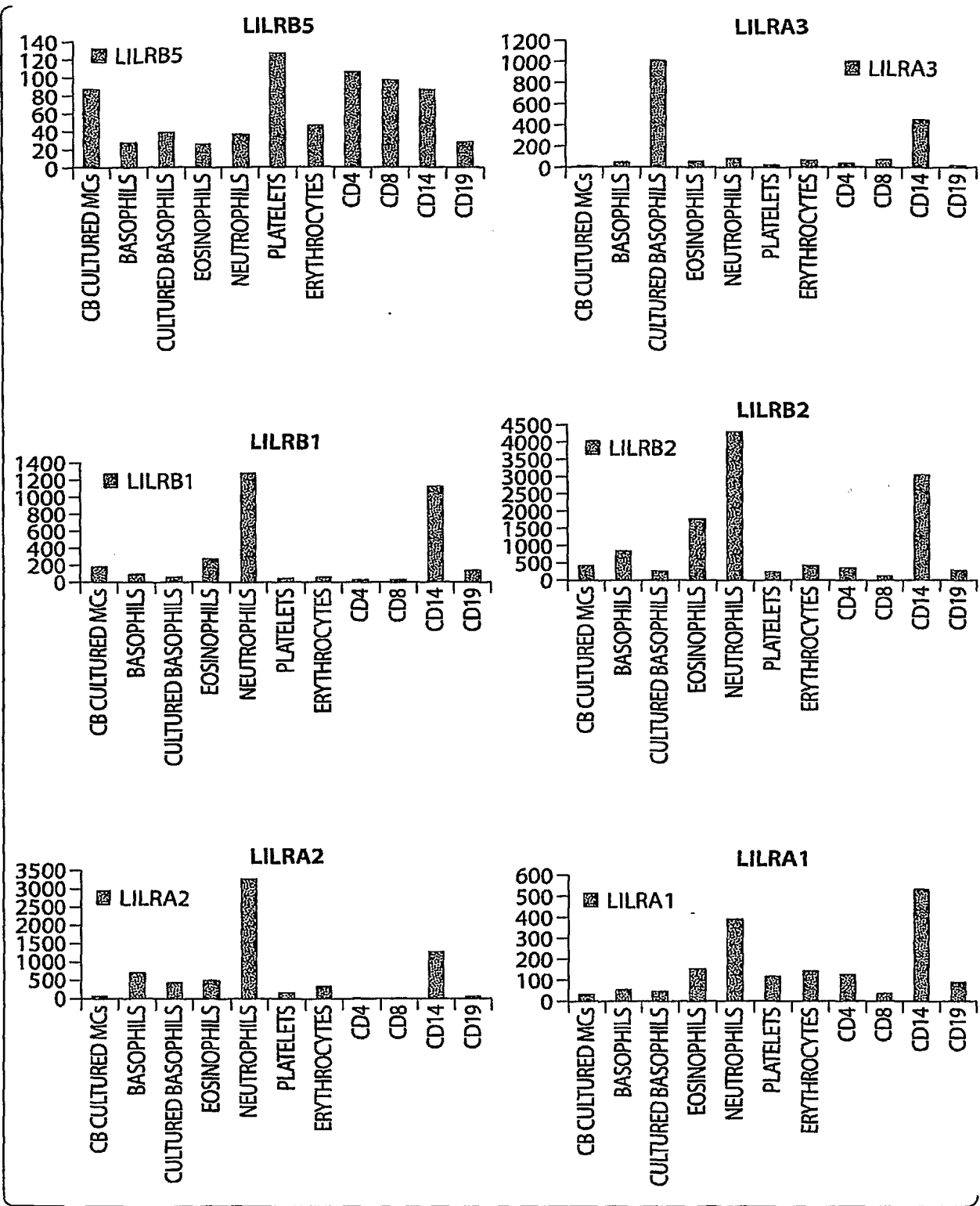


Fig. 5B

16/36

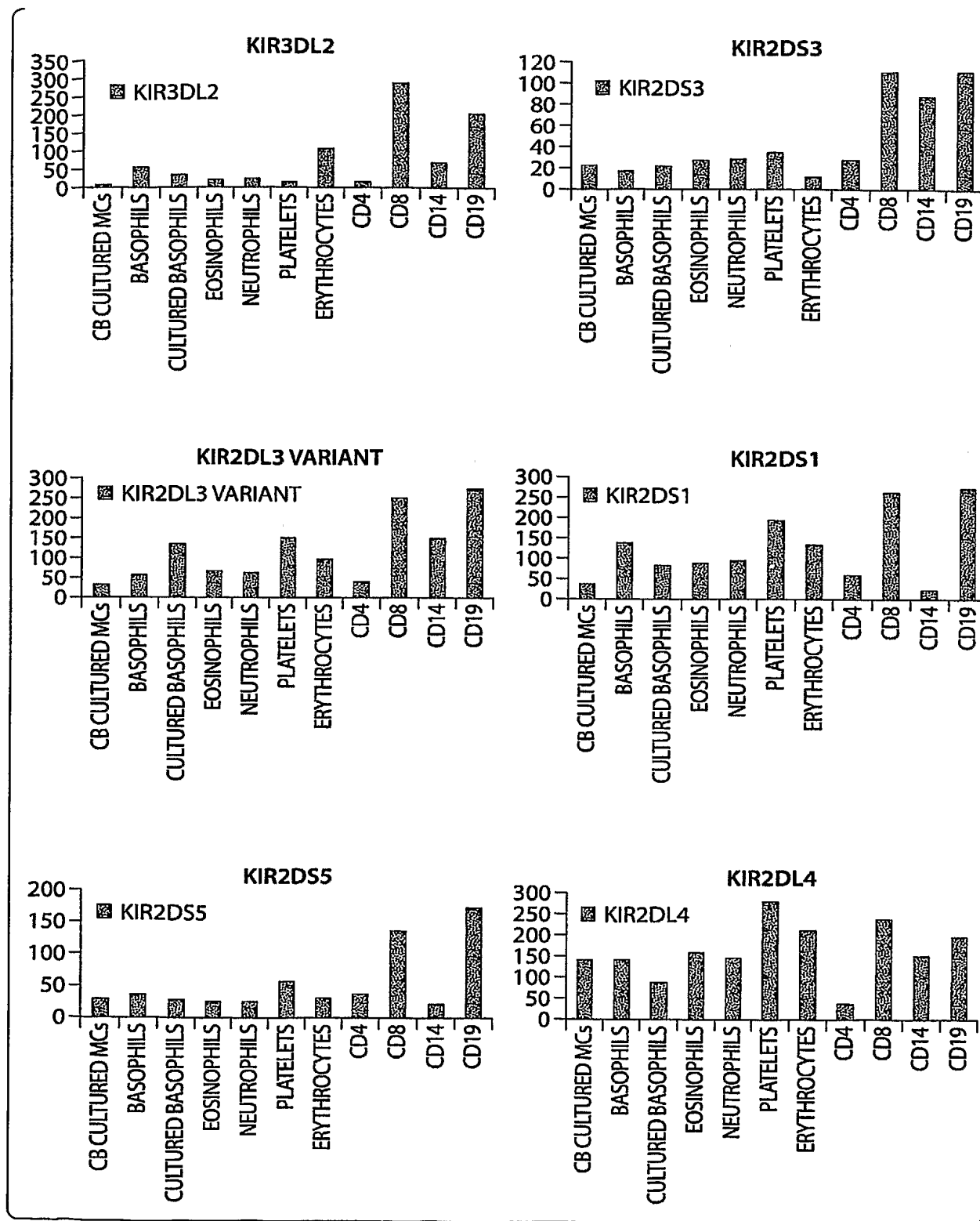


Fig. 5C

17/36

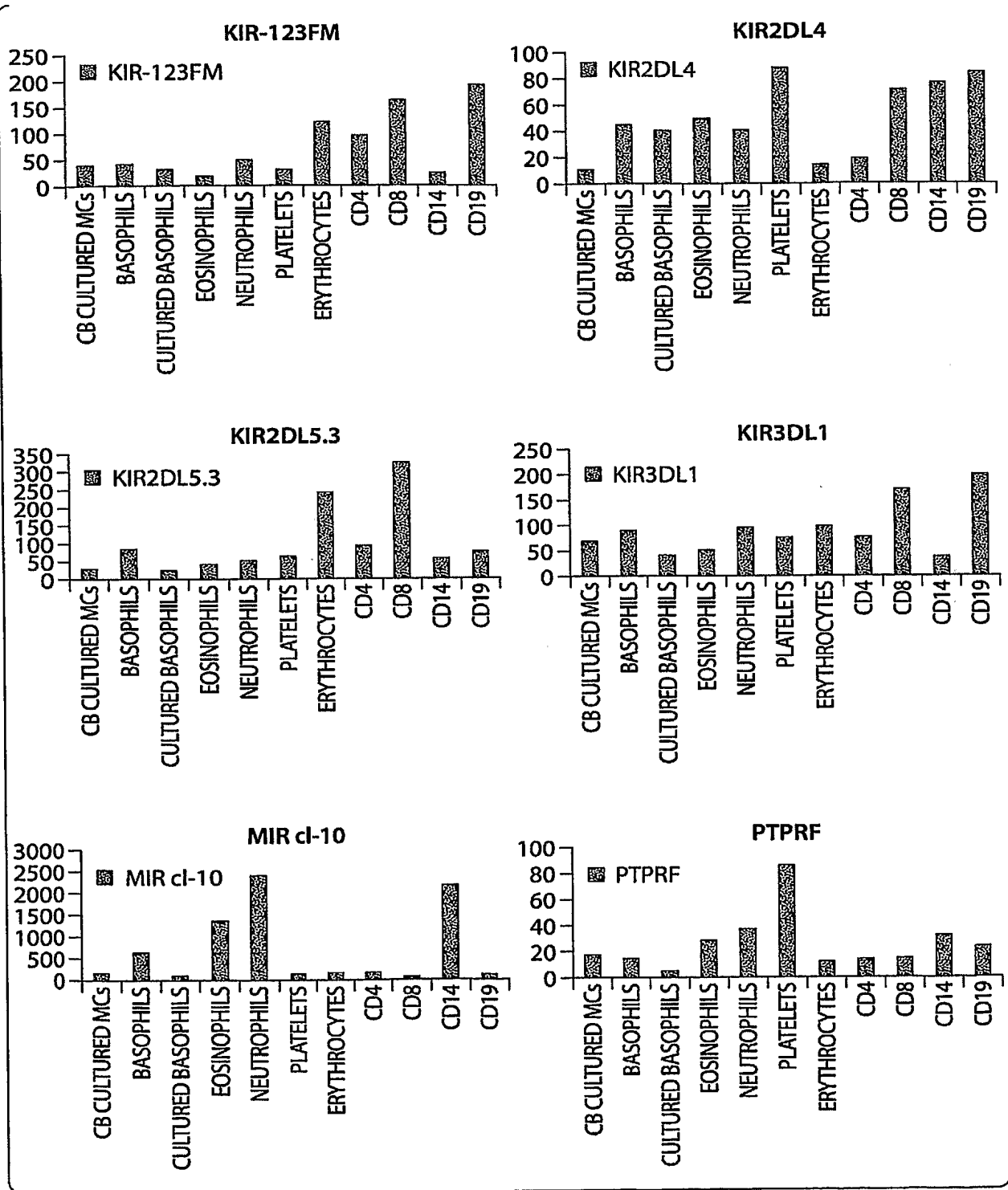


Fig. 5D

Table E1. The complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), CD4⁺ cells, CD8⁺ cells, CD14⁺ cells, CD19⁺ cells and nasal polyp-derived cultured fibroblasts (Fb). When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. Transcripts having S.I. >3-fold were shown in A-H. Abbreviations used in the table through A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

A. Basophil (Ba)-selective transcripts (1/2).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	EO 1	EO 2	EO 3 (small)	EO 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl (small)	CD4	CD8	CD14	CD19	Fb	Ba S.I.
207539_s_at	NM_000589.1	IL-4	0.2	0.1	10.4	16.9	13.4	0.1	0.0	0.2	0.1	0.1	0.3	0.0	1.2	0.2	0.0	0.2	0.1	0.0	0.0	73348
210254_at	L35948.1	HTrm4	0.8	0.4	115.6	130.1	153.6	2.4	1.7	21.8	1.7	0.1	0.9	3.6	9.5	0.2	0.5	0.4	0.1	0.2	0.0	3824
205513_at	NM_001062.1	vitamin B12 binding protein	1.5	1.2	98.9	149.3	110.9	3.2	2.2	16.1	1.9	4.9	4.5	6.3	8.1	1.8	0.7	0.8	1.4	0.9	0.1	20322
206148_at	NM_002183.1	IL-3 R	1.0	0.1	6.2	80.2	71.3	1.7	1.7	1.8	2.9	0.3	0.4	0.2	1.9	0.2	0.3	0.2	0.7	0.1	0.1	1662
214920_at	R33964	FLI11022 fis	0.1	1.1	4.9	13.1	15.4	0.1	0.2	0.7	0.5	1.0	0.4	0.5	0.7	0.1	0.1	0.2	0.1	0.3	0.1	16049
201825_s_at	AL572542	CGI-49	3.3	1.6	21.4	74.9	46.5	2.1	1.2	0.1	1.2	0.1	0.1	0.2	0.1	1.3	0.7	1.7	1.4	0.8	2.8	15045
213238_at	A1478147	ATPase, Class V, type 10D	1.2	2.9	39.9	76.3	118.9	2.3	1.7	3.1	1.9	2.1	1.4	2.3	6.8	0.7	0.9	0.9	2.5	5.0	4.1	14398
211734_s_at	BC005912.1	Fc epsilon RI alpha	10.5	28.4	210.0	220.8	226.2	8.4	2.1	4.8	2.9	0.3	0.7	4.5	16.6	1.4	5.1	0.8	1.4	0.4	0.2	12703
213894_at	BF447246	KIAA0950	0.1	0.0	3.7	13.0	15.6	0.3	0.4	0.4	0.4	0.9	0.7	0.7	0.6	0.5	0.6	0.1	0.1	0.2	0.2	12272
206363_at	NM_005360.2	c-MAF	3.7	1.4	36.5	75.7	66.4	1.2	0.1	0.2	0.2	0.2	0.1	0.2	1.0	0.6	4.8	2.7	0.5	1.0	0.0	11927
203373_at	NM_003877.1	SOC52	2.1	3.9	21.7	85.0	112.2	4.6	4.7	9.4	6.5	0.7	1.2	0.3	2.5	1.6	3.2	3.5	0.8	0.9	3.6	98282
207538_at	NM_000589.1	IL-4	0.3	0.1	5.4	9.8	9.2	0.4	0.4	0.0	0.3	0.1	0.0	0.4	0.7	0.8	0.4	0.3	0.1	0.0	0.1	98156
213684_s_at	BF671400	LIM-protein	0.6	0.1	11.1	21.0	20.6	1.9	1.6	2.4	1.8	0.8	0.6	1.5	2.5	0.1	0.0	0.3	1.0	0.0	0.1	89245
209360_s_at	D43968.1	AML1b protein	10.4	2.4	53.2	131.1	90.5	8.5	7.0	13.8	11.3	0.5	0.5	0.5	4.2	1.3	4.1	5.9	1.3	2.5	3.1	87543
220234_at	NM_004056.2	carbonic anhydrase VIII	0.4	0.1	11.7	10.2	6.0	1.2	0.1	0.2	0.4	0.8	0.9	0.1	0.5	0.5	1.1	0.1	0.1	0.1	0.8	81309
210643_at	AF053712.1	osteoprotegerin ligand	0.1	0.3	1.8	3.4	6.0	0.7	0.4	0.3	0.2	0.4	0.1	0.3	0.1	0.1	0.3	0.4	0.3	0.2	0.2	76628
209211_at	AF132818.1	colon Kruppel-like factor	0.1	0.0	1.8	10.2	8.8	0.3	0.5	1.5	0.8	1.1	0.7	0.8	0.5	0.2	0.2	0.4	0.2	0.1	0.3	7239
204309_at	NM_000781.1	CYP11A	0.3	0.1	2.6	6.1	5.6	0.1	0.3	0.5	0.5	1.0	0.1	0.1	0.9	0.3	0.3	0.1	0.0	0.3	0.7	68366
203372_s_at	AB004903.1	SOC52	0.6	1.6	9.2	8.5	15.9	1.4	2.4	0.9	0.2	0.7	0.6	0.4	0.8	0.8	1.6	1.3	0.3	0.3	1.4	68271
207463_x_at	NM_002771.1	serine protease 3 (trypsin 3) acid sphingomyelinase-like	1.0	1.0	4.8	10.0	10.9	0.4	1.0	1.0	1.2	1.2	0.9	1.0	1.8	0.4	0.6	0.4	0.3	0.7	1.2	67218

Fig. 6A-1

19/36

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pI	CD 4	CD 8	CD 14	CD 19	Fb	Ba S.L.
213624_at	AA873600	phosphodiesterase	4.7	2.0	20.8	30.6	25.9	2.1	2.8	3.8	1.7	0.5	1.1	1.3	1.3	0.1	0.2	0.1	3.8	0.2	3.2	6.6846
214873_at	AL137651.1	clone DKF7p434O0213	0.1	0.4	3.7	15.5	24.4	2.0	0.9	2.5	2.3	0.2	0.1	0.7	0.6	0.1	1.1	1.5	0.5	0.6	0.7	6.2585
204928_s_at	NM_019848.2	protein P3	2.3	1.5	9.8	49.0	34.3	3.7	3.3	4.8	4.2	1.6	1.0	1.9	2.2	4.1	1.8	3.0	0.8	2.0	2.6	6.2142
208935_s_at	L78132.1	prostate carcinoma tumor antigen (pcta-1)	2.2	1.2	9.9	19.1	16.6	2.3	1.5	3.6	2.5	1.1	1.1	1.9	0.9	1.8	1.8	2.0	2.0	1.4	0.8	6.2011
203201_at	NM_000303.1	phosphomannomutase 2 (PMM2)	1.8	0.3	10.7	15.9	6.5	0.9	0.6	1.2	0.9	0.8	0.4	1.1	1.3	1.0	1.3	1.2	1.2	1.1	1.7	6.1557
201826_s_at	NM_016002.1	CGI-49	1.8	3.1	11.0	27.5	15.1	1.6	1.1	1.4	2.1	1.1	1.4	1.3	1.8	1.6	1.1	1.1	1.1	0.6	2.9	5.6407
213421_x_at	AW007273	serine protease 4 (trypsin-4)	1.8	1.7	5.9	12.5	11.4	1.0	0.5	1.2	0.5	1.2	1.7	1.2	1.2	0.9	1.0	1.2	1.0	0.4	1.7	5.4082
209348_s_at	AF055376.1	c-MAF, short form	6.4	4.9	29.6	47.7	42.3	0.8	0.3	0.4	0.6	0.3	0.0	0.9	1.4	1.0	7.3	3.1	0.9	0.7	1.4	5.3183
213343_s_at	AL041124	hypothetical protein PP1665	0.9	0.2	12.2	17.0	12.0	3.5	1.7	0.5	0.6	0.1	0.3	0.8	0.4	0.6	1.5	2.6	0.7	1.6	1.3	5.2721
202491_s_at	NM_003640.1	Ikappa B-associated protein	1.6	3.8	23.9	51.9	43.5	4.6	4.0	7.1	7.3	1.6	2.1	2.5	2.3	1.7	3.7	7.4	3.2	4.7	4.2	5.107
221021_s_at	NM_030877.1	Bos taurus P14 protein	6.9	3.2	7.2	29.2	58.9	2.8	3.2	5.4	6.3	0.9	1.2	7.8	1.6	1.6	2.2	2.4	2.0	3.5	1.8	4.9129
213346_at	BE748563	hypothetical protein BC015148	2.7	1.8	17.5	38.8	25.8	4.0	6.7	6.2	4.8	1.4	0.9	0.8	1.1	0.2	1.2	1.5	0.6	1.1	1.9	4.8879
209764_at	AL022312	mannosyl (beta-1,4)-glycoprotein	0.0	0.9	4.1	6.1	5.8	0.8	1.4	0.9	1.4	0.6	0.1	0.5	0.2	1.0	0.4	0.2	0.2	0.4	0.3	4.855
207067_s_at	NM_002112.1	beta-1,4-N-acetylglucosaminyltransferase	64.1	14.7	105.2	164.9	165.7	3.4	1.4	4.1	2.8	2.1	1.2	4.6	14.0	2.4	0.8	0.9	1.7	0.7	0.2	4.6305
210375_at	X83858.1	histidine decarboxylase	1.0	0.6	2.4	11.5	17.0	0.3	0.1	0.1	0.0	0.4	0.7	0.9	0.7	0.6	0.3	0.2	0.2	0.5	1.7	4.6103
206306_at	NM_001036.1	prostaglandin E receptor, type 3a2	2.1	1.1	3.7	11.0	7.8	1.0	0.6	1.5	0.5	1.2	0.3	1.5	0.9	1.1	0.7	0.3	1.0	0.2	0.4	4.5552
210001_s_at	AB005043.1	ryanodine receptor 3 (RYR3)	5.2	0.2	3.0	24.1	29.9	2.1	3.0	3.2	3.4	0.3	1.0	0.8	1.3	0.8	0.8	0.8	0.0	0.8	0.9	4.5248
		SOC51																				
		serine (or cysteine) proteinase inhibitor,																				
		clase B (ovalbumin), member 2																				
204614_at	NM_002575.1	(SERPINB2)	0.3	0.6	5.3	12.9	12.5	0.4	2.4	4.2	2.0	1.0	0.8	0.7	0.3	1.9	0.5	0.7	2.1	0.2	0.2	4.5061
209940_at	X16323.1	hepatocyte growth factor (HGF)	0.4	0.0	2.3	7.3	5.5	0.5	0.4	0.6	0.5	0.1	0.1	1.0	0.6	0.7	0.1	0.0	1.0	0.0	0.5	4.4335
209212_s_at	AB030824.1	transcription factor BTEB2	0.1	0.2	7.5	14.3	22.1	2.3	2.0	4.9	3.7	1.2	1.3	1.5	2.5	1.4	0.5	0.2	1.1	0.9	0.8	4.363

Fig. 6A-2

20/36

A. Basophil (Ba)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC	MC	Ba1	Ba2	Ba3	EO	EO	EO3	EO4	Ne	Ne	Ne3	Ne4	CD4	CD8	CD14	CD19	Fb	BaSL
214651_s_at	U41813.1	class 1 homeoprotein (HOXA9)	0.6	0.6	1.7	6.3	8.3	0.3	0.5	0.8	0.5	0.1	0.1	0.5	1.0	0.1	0.1	0.3	0.1	0.1	4.3618
32502_at	AL041124	DKFp34D0316_s1	1.6	1.9	14.6	22.5	17.4	4.0	2.1	0.7	1.4	1.1	1.0	0.4	0.4	2.3	2.5	4.1	2.5	2.3	4.3594
205373_at	NM_004389.1	catenin (cadherin-associated protein)	0.2	0.1	1.1	3.9	3.2	0.6	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.6	0.2	0.2	4.2308
219676_at	NM_025231.1	alpha 2	0.3	0.7	2.5	7.3	12.0	0.9	0.2	2.0	1.5	0.2	1.1	4.2	2.2	0.6	1.1	0.4	0.3	1.4	4.2135
213385_at	AK026415.1	beta2-chimaerin	4.7	3.1	8.3	22.9	21.8	1.1	0.8	0.9	0.9	0.2	1.5	0.8	1.0	0.1	0.9	1.6	3.3	0.2	4.2131
214637_at	BG437034	oncostatin M	0.4	0.0	0.9	5.4	4.4	0.2	0.7	0.1	0.7	0.5	1.8	0.2	1.1	0.4	0.1	0.1	0.2	0.1	4.1983
202416_at	AF153419.2	leptin B-associated protein	0.2	0.2	1.3	3.6	2.2	0.4	0.4	0.5	0.1	0.0	0.0	0.2	0.0	0.3	0.3	0.5	0.2	0.4	4.1747
20416_at	NM_024837.1	FLJ1472	4.1	1.5	9.1	9.7	12.2	1.9	3.3	3.0	1.9	0.8	0.6	1.1	0.9	0.7	0.6	0.2	0.8	0.3	4.1718
218318_s_at	NM_016231.1	renin-like kinase	1.4	1.3	6.2	7.0	7.1	0.8	0.9	0.8	0.6	0.5	1.0	0.1	0.1	1.6	1.3	0.9	1.2	1.1	4.1558
215201_at	AW166925	FLJ14135 fs clone MAMMA1002728	0.6	0.1	0.1	2.1	3.5	0.5	0.7	0.8	0.9	0.0	0.1	0.1	0.1	0.1	0.5	0.3	0.8	0.4	4.0555
222303_at	AV700891	ETS2 intronic transcript 1 mRNA	0.6	1.4	31.1	86.8	63.8	3.6	2.2	2.9	3.2	10.8	10.5	16.6	19.0	1.2	0.7	0.7	8.1	0.3	4.0555
201664_at	AL136877.1	DKFp34F205	2.8	5.0	17.3	27.7	31.8	4.4	5.3	9.1	8.3	4.3	3.9	5.7	5.5	0.1	4.8	4.2	2.5	4.1	3.8471
210252_s_at	AB002356.1	MAP-kinase activating death domain	5.6	4.6	12.7	35.0	40.7	6.2	6.1	7.0	8.3	2.2	1.3	1.9	3.3	5.2	2.7	5.4	3.0	3.5	3.8424
201328_at	AL575509	v-ets avian erythroblastosis virus E26	1.7	0.1	18.4	34.7	50.7	2.8	1.6	1.7	1.8	6.4	9.9	8.7	8.9	0.5	0.9	1.0	4.4	0.1	3.8075
218392_x_at	NM_022754	oncogene homolog 2	1.2	1.0	3.5	7.5	7.4	1.4	1.0	2.7	1.5	1.0	0.6	0.9	0.1	0.9	1.4	0.4	0.7	0.5	3.7693
205046_at	NM_001813.1	FLJ12876	0.0	0.3	1.5	8.1	13.1	1.7	0.5	1.9	1.2	0.5	1.3	1.0	0.9	1.1	1.5	0.9	1.0	0.4	3.7324
221170_at	AF122301.1	histamine H4 receptor	0.6	0.8	35.9	34.2	32.5	7.8	11.9	8.7	9.3	0.2	0.8	0.8	1.0	0.4	0.8	0.5	0.6	0.0	3.6719
201663_s_at	NM_005496.1	chromosome-associated polypeptide C	2.2	4.3	17.6	15.1	18.1	3.4	6.6	4.9	4.2	4.0	3.7	2.2	2.7	1.7	4.1	2.9	1.7	3.7	3.6472
208933_s_at	AL659005	lectin, galactoside-binding, soluble, 8	11.8	4.9	26.7	28.3	28.2	5.9	6.6	10.1	4.8	3.8	4.5	5.5	2.1	4.3	7.6	7.4	7.2	4.3	3.6311
209710_at	AL563460	(galectin 8)	50.4	38.9	141.1	189.2	154.7	4.4	1.3	3.8	3.1	0.7	1.2	5.4	10.8	2.5	0.7	0.9	0.3	0.1	3.6251
205769_at	NM_003645.1	fatty acid-Coenzyme A ligase, very	3.3	2.5	7.0	16.2	9.2	0.3	0.3	0.3	0.5	0.1	0.4	0.2	0.3	0.2	0.4	0.7	0.1	0.3	3.5389
209409_at	D86962.1	long-chain 1 (FACUL1)	8.4	2.6	12.5	38.0	33.1	4.9	4.2	12.3	10.4	1.7	1.7	2.1	1.8	1.4	0.4	0.7	1.5	0.4	3.4907
38398_at	AB002356	KIAA0207	5.5	4.1	13.8	24.6	29.8	6.1	6.4	5.6	7.0	3.0	3.2	3.3	4.1	5.1	3.3	5.3	3.7	4.4	3.4534
205899_at	NM_003914.1	KIAA0358	5.6	3.6	16.2	20.6	10.5	0.1	0.6	0.9	0.1	1.6	0.1	0.8	0.4	1.9	0.7	0.1	0.1	0.3	3.3824
218150_at	NM_012097.1	cyclin A1	8.2	5.3	37.6	56.6	54.6	9.1	8.6	14.0	3.1	3.9	5.0	7.7	9.6	3.8	8.3	8.1	14.5	9.9	3.3745
213097_s_at	A338837	ADP-ribosylation factor-like 5	2.1	1.8	8.4	13.4	16.7	4.8	2.1	4.8	3.7	1.8	1.2	1.2	1.6	0.3	3.4	3.7	2.3	3.3	3.3672
208158_s_at	NM_018030.1	zuculin related factor 1	1.2	2.3	8.8	18.0	15.3	0.6	0.8	1.6	1.4	1.5	2.3	2.7	1.8	2.0	0.2	0.7	1.3	0.5	3.342
210109_at	AF191492.1	oxysterol-binding protein-related protein	1.2	0.7	3.6	6.4	4.2	1.2	1.6	1.0	0.3	0.6	1.1	1.7	0.6	0.2	1.3	0.5	1.4	0.6	3.2977
220918_at	NM_025143.1	nasopharyngeal carcinoma associated gene protein-8	1.0	1.1	26.1	37.3	26.2	6.2	6.5	14.1	11.3	3.3	2.5	2.0	2.0	1.1	0.9	0.9	3.5	1.1	3.2902
209359_x_at	L34598.1	aml 1 (acute myeloid leukemia 1)	1.2	0.1	3.1	7.2	7.1	2.5	1.6	1.6	1.1	0.2	1.0	0.6	1.4	0.7	0.7	1.0	0.8	0.6	3.2789
208107_s_at	NM_030941.1	oncogene	3.6	7.6	7.8	30.6	20.1	1.6	2.3	2.7	0.8	0.6	0.2	1.5	1.0	0.2	0.1	0.3	0.2	0.1	3.2356
212412_at	AV715767	exonuclease NEF-sp	18.2	16.2	41.3	72.5	67.3	7.7	7.7	16.3	11.6	6.4	6.3	9.1	12.7	3.7	3.1	4.1	8.0	3.3	3.2017
215215_s_at	AC004381	DKFp564A072	2.9	2.5	4.8	12.8	10.4	0.6	0.9	1.4	0.8	0.1	0.0	0.2	0.8	0.1	0.4	0.3	0.4	0.3	3.198
221509_at	AB014731.1	chromosome 16 BAC clone	7.6	5.4	13.2	48.5	32.4	5.2	5.7	18.1	10.7	3.5	3.8	11.4	8.1	2.8	5.6	6.0	4.1	7.5	3.1618
218637_at	NM_018439.1	SNAP-3	1.3	2.4	2.9	10.7	9.3	1.5	1.5	2.7	2.1	0.6	0.7	0.6	0.6	1.2	0.8	0.7	0.9	1.1	3.1587
218352_at	NM_018191.1	hypothetical protein IMPACT	0.8	0.5	4.9	13.7	8.7	2.3	1.7	3.4	3.9	1.0	2.0	2.8	3.6	0.8	2.3	2.0	1.7	2.2	3.1058
213035_at	A081194	hypothetical protein FLJ10716	2.1	3.8	11.1	26.7	22.4	2.5	1.5	3.4	2.5	1.9	1.1	2.3	1.6	4.6	2.5	1.3	0.1	2.2	3.0937
211180_x_at	D89788.1	KIAA0379	1.5	0.2	3.1	9.4	7.5	2.0	2.5	1.7	1.7	1.0	1.4	0.3	1.1	0.4	0.4	0.6	1.1	0.7	3.0936
210731_s_at	AL136105	aml 1 (acute myeloid leukemia 1) oncogene	2.1	1.1	4.8	9.1	6.4	1.9	1.8	3.0	1.8	1.2	1.4	2.7	1.6	2.1	1.2	1.2	1.7	1.3	3.0876
203164_at	BE464756	(galectin 8)	2.3	1.9	3.7	12.6	12.4	2.5	1.9	4.0	2.7	1.1	0.6	1.2	1.7	1.4	2.3	2.6	2.1	2.7	3.063
205768_s_at	NM_003645.1	acetyl-Coenzyme A transporter	3.0	1.7	3.9	10.7	7.7	0.4	0.1	0.6	0.2	0.1	0.8	0.1	0.7	0.0	0.8	0.1	0.2	0.1	3.0353
210517_s_at	AB003476.1	fatty acid-Coenzyme A ligase very long-chain 1 (FACVL1)	25.1	4.9	44.0	69.5	59.6	1.5	0.4	0.6	0.8	0.1	0.2	1.0	3.0	0.9	0.8	0.5	0.1	0.3	3.0146
210647_x_at	AF102988.1	A kinase (PRKA) anchor protein (gravin) 12	2.3	1.1	18.7	13.2	9.1	3.4	3.3	4.0	4.5	3.3	5.0	4.2	3.6	1.8	3.5	4.4	1.8	2.8	3.002
		Ca2+-independent phospholipase A2 short isoform																			

Fig. 6B

21/36

B. Eosinophil (Eo)-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC	cord blood	MC	Ba1	Ba2	Ba3	Eo	Eo3	Eo4	Ne	Ne3	Ne4	p1	CD4	CD8	CD14	CD19	Fb	FoSL		
207328_at	NM_001140.1	15-lipoxygenase	0.1	0.6	0.7	0.1	0.1	14.5	24.6	18.3	17.0	0.1	1.1	0.1	0.1	0.1	0.0	0.1	0.0	0.1	0.0	74.129	
2129695_at	NM_024703.1	FLJ2593	0.0	1.0	1.8	1.8	1.1	29.8	34.7	24.8	27.8	0.8	1.5	0.4	0.9	0.1	0.6	0.4	0.3	0.1	0.1	19.123	
208253_at	NM_014442.1	salic acid binding Ig-like lectin, Siglec B	1.3	2.4	0.4	0.4	0.2	17.1	23.1	17.6	11.8	0.1	0.4	0.1	0.8	0.3	0.2	0.1	0.2	0.5	0.2	9.8056	
211922_s_at	AV028632.1	catalase	3.7	2.2	6.2	6.8	2.2	78.2	134.5	119.7	88.8	16.2	13.0	8.8	8.7	0.7	2.2	2.9	11.1	7.5	4.6	9.125	
201802_at	NM_004955.1	solute carrier family 29 (nucleoside transporters)	4.8	2.8	2.9	3.4	1.9	24.8	30.4	36.1	42.3	0.1	0.6	0.6	0.8	0.2	0.9	0.3	2.2	1.0	1.1	8.989	
21214523_at	NM_001805.1	CCAAT enhancer binding protein (CEBP), epsilon	0.1	0.1	0.7	1.2	1.2	7.9	11.4	23.4	17.3	1.8	1.5	1.9	1.1	1.4	0.5	0.4	1.0	0.1	0.1	8.9462	
21210029_at	M34455.1	interferon-gamma-inducible indoleamine 2,3-dioxygenase	0.7	0.1	5.3	4.2	2.6	20.0	39.0	33.4	29.5	1.6	2.1	2.3	1.8	1.7	1.5	1.7	0.3	1.4	0.9	7.7078	
2115573_at	AU147084	FLJ12072	0.1	0.1	0.5	0.3	1.1	9.8	8.4	16.9	7.2	0.4	1.9	1.8	2.0	0.1	0.1	0.0	0.1	0.4	0.0	7.5983	
201801_s_at	AF079117.1	solute carrier family 29 (nucleoside transporters)	3.5	1.9	1.7	0.5	0.9	29.7	47.1	7.4	11.0	0.1	0.5	0.4	0.7	1.1	0.4	0.1	1.4	0.6	1.0	7.0314	
2113825_at	AF221520.1	oligodendrocyte lineage transcription factor 2	0.4	0.6	0.2	0.4	0.6	6.0	10.9	18.7	12.5	0.8	0.9	1.5	1.0	0.6	1.7	0.3	0.4	0.3	0.3	6.5987	
2119821_s_at	NM_018988.1	glucose-fructose oxidoreductase domain containing	3.0	1.4	1.8	2.6	2.3	18.7	17.3	30.9	31.3	3.9	3.1	2.4	2.9	3.2	1.3	2.5	3.0	3.8	0.8	6.2284	
205472_s_at	NM_004392.1	dachshund (Drosophila) homolog	0.0	0.1	0.1	0.4	0.1	2.7	1.4	2.2	1.7	0.3	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.3	0.0	6.0088	
202188_at	NM_014669.1	KIAA0095	0.5	0.9	0.4	1.8	1.2	6.8	8.5	13.5	10.6	0.2	0.2	0.2	0.1	0.2	0.3	1.7	1.7	1.4	0.4	5.4499	
2110548_at	U58913.1	chemokine CCL23	0.6	1.8	0.4	1.1	0.5	5.5	6.2	4.2	6.9	0.1	0.9	0.1	0.2	0.3	0.1	0.2	0.6	0.1	0.0	5.3082	
209447_at	AF043290.1	lymphocyte membrane associated protein (BB7)	0.6	0.5	2.5	3.4	3.6	41.8	49.7	66.2	60.1	0.2	0.9	0.5	1.2	2.6	5.1	10.4	1.6	6.3	2.7	5.1472	
206171_at	NM_000677.2	ADORA3 adenosine A3 receptor	2.3	2.8	2.8	3.7	2.2	7.8	13.9	22.0	17.9	1.6	3.1	2.2	2.5	1.2	1.6	0.5	2.0	0.5	0.5	5.0469	
2110549_s_at	U58913.1	chemokine CCL23	1.1	1.1	0.1	1.3	0.6	7.9	5.6	2.7	8.1	0.0	0.6	0.0	0.2	0.1	0.1	0.1	0.2	0.0	0.4	4.9873	
21214183_s_at	X91817.1	transketolase-like protein	0.1	0.2	0.2	0.1	0.1	3.2	4.0	6.6	7.2	0.2	0.2	0.1	0.1	0.2	0.2	1.0	0.1	0.6	0.0	4.7894	
2115350_at	AB033088.1	spectrin repeat containing, nuclear envelope 1	0.1	0.1	0.5	0.1	0.1	3.8	4.2	3.0	2.8	0.0	0.1	0.2	0.4	0.7	0.2	0.1	0.0	0.1	0.2	4.7822	
206277_at	NM_002564.1	P2Y2 purinergic receptor	0.1	0.1	0.1	0.2	0.1	3.4	4.7	8.1	5.9	0.1	0.3	0.1	0.1	0.2	0.1	0.3	1.2	0.2	0.1	4.3043	
204776_at	NM_003248.1	thrombospondin 4 (THBS4)	0.8	0.1	1.5	0.1	0.8	3.2	5.9	10.0	6.4	1.8	1.4	0.6	0.9	0.3	0.2	0.3	1.4	1.1	1.2	4.1746	
201563_at	L29008.1	L-iditol-2 dehydrogenase	4.1	2.6	3.5	11.4	12.8	22.5	29.9	49.0	37.0	1.8	3.0	4.4	2.2	2.1	1.6	1.2	2.7	2.5	1.8	4.1557	
206637_at	NM_014879.1	P2YX purinergic receptor GPR105 for UDP-glucose	5.7	1.6	13.3	19.9	13.5	44.2	55.1	81.4	62.4	1.8	9.3	15.4	9.2	0.7	0.9	0.8	0.0	5.5	0.1	3.8761	
2113622_at	A1733465	collagen, type IX, alpha 2	1.5	1.4	1.9	1.2	1.3	10.3	9.6	6.6	8.8	2.7	2.1	2.1	2.2	0.7	1.2	1.2	2.2	1.7	0.9	3.8576	
21214705_at	A1011306.1	PDZ domain protein	0.1	0.1	0.4	0.3	0.1	2.1	1.5	2.6	2.2	0.3	0.0	0.6	0.7	0.1	0.4	0.3	0.3	0.6	0.1	3.6532	
266_s_at	L33930	CD24 signal transducer	0.2	0.1	3.0	0.3	0.8	11.9	14.0	18.8	13.9	0.1	0.1	0.3	0.8	0.9	0.0	0.1	0.1	0.1	0.1	3.3793	
201432_at	NM_001752.1	catalase (CAT)	23.0	14.3	35.7	49.4	19.9	20.3	20.7	221.6	207.3	67.0	54.3	71.3	60.9	9.2	11.2	15.1	53.6	29.9	21.4	3.3325	
209696_at	D26054.1	fructose-1,6-bisphosphatase	0.9	3.4	4.3	11.1	6.4	20.2	27.7	28.8	32.5	3.0	2.5	2.4	1.5	1.9	2.0	1.6	8.1	1.1	0.6	3.3089	
2116379_x_at	AK001168.1	CD24 signal transducer	1.3	1.4	16.2	0.9	1.5	66.1	70.1	81.9	77.9	1.7	2.8	2.6	4.1	4.8	0.5	0.6	0.9	22.5	0.5	3.2741	
205569_at	NM_014398.1	lysosome-associated membrane glycoprotein (TSC403)	0.4	0.2	0.7	0.1	0.4	2.4	3.1	6.8	3.0	0.6	0.1	1.4	0.8	0.4	1.1	0.7	0.1	0.0	0.3	3.2308	
2119233_s_at	NM_018653.0.1	hypothetical protein PRO2521	0.1	0.1	1.9	2.1	4.6	5.4	7.5	8.5	21.8	21.2	0.8	0.1	1.5	2.1	0.1	1.1	4.1	0.1	1.4	0.5	3.2093
202286_s_at	J04152	gastrointestinal tumor-associated antigen GAT33-1	0.9	0.7	1.3	0.3	0.1	1.1	2.5	8.7	1.8	0.4	0.8	0.6	0.6	0.2	0.2	0.7	0.3	0.5	0.1	3.1844	
206442_at	NM_003007.1	semenogelin I (SEMG1)	0.6	0.1	0.4	0.0	0.1	1.2	3.2	4.9	3.4	0.3	0.2	1.1	1.9	0.1	0.2	0.2	0.9	0.4	0.1	3.1837	
205733_at	NM_000057.1	Bloom syndrome	1.9	1.1	2.0	2.4	2.2	8.5	6.0	7.5	11.2	2.1	2.0	1.0	1.2	1.2	2.4	1.8	1.1	2.6	1.2	3.1427	
204392_at	NM_003656.2	calcium/calmodulin-dependent protein kinase I (CAMK1)	4.0	1.1	6.3	8.9	6.4	17.8	19.3	24.9	26.5	0.6	0.2	1.8	1.5	0.1	1.4	1.0	3.0	0.6	1.8	3.0763	
2113497_at	AL050374.1	DKFZp586C1619	1.0	0.7	1.0	1.3	1.6	6.3	6.8	6.8	6.0	2.3	3.0	1.4	2.3	2.0	0.4	0.5	1.6	1.1	0.8	3.0099	
2119296_at	NM_019028.1	similar to ankyrin repeat-containing protein ANK1	2.2	1.7	0.2	3.5	1.6	7.3	4.4	8.4	7.4	1.8	2.4	2.4	2.3	0.1	1.4	1.6	1.3	1.9	0.8	3.0018	

Fig. 6C

22/36

C. Neutrophil (Ne)-selective transcripts (1/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1	Ba2	Ba3	EO	EO	EO	EO3	EO4	Ne	Ne	Ne3	Ne4	pL	CD4	CD8	CD14	CD19	Fb	NeSL
205403_at	NM_004633.1	Interleukin 1R type II	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.4	0.1	0.2	0.0	0.0	12.86
216782_at	AK026679.1	FLJ23026 fts	0.0	0.2	0.2	0.1	0.1	0.1	0.1	0.1	0.5	0.2	0.2	0.2	0.2	0.2	0.1	0.1	0.1	0.1	0.2	0.2	112.28
210119_at	U73191.1	ICN	0.7	1.1	0.1	0.1	0.5	0.1	0.1	0.1	0.9	0.6	81.6	98.6	129.0	88.8	0.7	0.2	0.0	0.8	0.0	0.0	107.47
209395_at	M80927.1	channel Kir1.3 chitinase 3-like 1 (cartilage glycoprotein-39)	1.5	0.2	0.9	0.1	0.4	0.3	0.1	0.1	8.1	0.1	28.9	25.3	70.7	40.7	0.1	0.0	0.1	0.1	0.1	0.0	79.595
203691_at	NM_002638.1	protease inhibitor 3, skin-derived (SKALP)	0.2	0.1	0.1	0.1	0.8	0.5	0.2	0.4	0.4	0.1	16.9	36.7	27.7	24.5	0.1	0.1	0.1	0.1	0.5	0.1	51.901
211372_s_at	U64094.1	Interleukin 1R type II	0.1	0.2	0.1	0.1	0.0	0.1	0.5	0.7	0.7	0.1	21.6	36.5	31.4	29.9	0.3	0.2	0.0	0.6	0.0	0.0	50.606
207008_at	NM_001557.1	CXCR2 Interleukin B receptor, beta	0.0	0.4	1.1	1.2	1.0	1.3	1.3	2.1	2.1	1.2	129.8	168.4	81.5	68.8	2.7	0.3	0.8	0.7	0.6	0.0	39.316
206515_at	NM_000896.1	leukotriene B4 omega hydroxylase (CYP4F3)	0.3	0.1	1.1	0.7	1.2	0.5	0.8	5.9	5.9	1.7	56.8	40.3	57.2	48.9	0.2	0.9	0.0	0.7	0.3	0.3	34.919
204007_at	J04162.1	Fc gamma R IIb (CD16)	0.8	0.7	1.4	1.5	1.8	1.1	1.8	2.8	2.8	1.9	204.5	226.5	194.0	173.3	6.6	1.3	1.3	2.2	2.6	0.1	29.895
204470_at	NM_001511.1	melanoma growth stimulating activity, alpha	1.2	0.0	0.7	0.9	0.1	0.6	0.5	1.2	1.2	0.7	19.1	23.0	26.3	48.1	0.1	0.2	0.2	1.0	0.1	0.2	28.189
206025_s_at	AW188198	tumor necrosis factor, alpha-induced protein 6	0.1	0.3	0.1	0.6	0.4	0.6	0.1	0.2	0.2	0.1	19.0	29.9	17.2	24.7	0.1	0.2	0.2	0.8	0.3	0.6	26.336
209396_s_at	M80927.1	chitinase 3-like 1 (cartilage glycoprotein-39)	1.8	0.2	1.6	0.4	0.5	0.8	0.5	5.6	5.6	0.9	37.9	32.2	52.8	26.7	1.4	0.0	0.0	0.1	0.1	0.4	25.669
211806_s_at	D87291.1	ICN	0.9	1.7	2.0	1.4	1.4	2.1	1.3	1.8	1.8	1.7	62.2	77.2	77.5	56.8	3.0	1.0	1.1	1.7	0.9	0.7	22.254
221920_s_at	B6577761	channel Kir1.3	0.4	0.8	0.9	0.0	0.2	2.4	1.5	2.2	2.2	1.5	59.0	43.2	57.4	46.8	2.5	0.7	0.3	1.8	1.1	1.0	20.163
207094_at	NM_000634.1	mitochondrial solute carrier	0.3	0.1	4.2	4.3	4.4	0.3	0.3	0.2	0.2	0.3	69.2	81.9	95.3	87.4	0.4	0.3	0.2	0.2	0.1	0.1	19.325
213589_s_at	AW468201	alpha	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.2	0.1	5.5	2.7	5.1	4.0	0.1	0.1	0.2	0.1	0.1	0.0	18.973
218963_s_at	NM_015515.1	DKFZP434G032	0.0	0.1	0.5	0.3	0.1	1.1	2.8	2.8	2.8	2.0	46.3	32.5	40.3	31.3	0.3	0.3	0.1	0.1	0.1	0.1	18.3
213506_at	B656369	PAR2 proteinase activated receptor-2	0.1	0.0	0.0	0.4	0.3	1.2	1.3	4.1	4.1	2.3	33.4	35.7	42.4	33.4	0.1	0.7	0.1	1.6	0.4	1.2	18.208
220187_at	NM_024636.1	FLJ2153	0.3	0.1	0.3	0.1	0.1	0.0	0.1	0.5	0.5	0.5	16.5	26.3	5.7	7.0	0.0	0.1	0.1	0.7	0.1	0.2	17.111
206026_s_at	NM_007115.1	tumor necrosis factor, alpha-induced protein 6	0.1	0.8	0.4	0.8	0.6	1.1	0.5	0.9	0.9	0.1	18.2	23.3	20.0	17.0	0.6	1.0	1.0	1.1	0.1	1.0	17.051
41469_at	L10343	elafin	1.2	0.7	1.2	0.8	0.8	0.9	1.0	0.7	0.7	0.8	16.2	39.1	19.5	17.4	1.3	1.4	0.7	0.8	0.5	0.5	15.913
205568_at	NM_020980.2	aquaporin 9	0.5	0.9	0.1	0.1	0.1	0.3	0.1	1.0	1.0	0.1	133.3	136.7	169.0	110.5	0.4	0.9	0.1	8.6	0.1	0.2	15.805
210483_at	BC005043.1	decoy receptor 1, TRAILR3	0.1	0.1	0.1	0.1	0.7	1.0	0.9	1.3	1.3	1.2	25.8	23.2	9.7	8.6	0.2	0.4	0.3	0.2	0.2	0.1	13.337
215223_s_at	W46388	superoxide dismutase 2	4.4	1.9	1.7	4.9	8.7	5.8	3.3	6.0	6.0	8.3	124.6	153.1	142.4	151.8	11.0	1.6	1.1	7.3	2.2	1.5	13.008
210484_s_at	BC005043.1	decoy receptor 1, TRAILR3	0.9	0.9	0.9	0.2	0.1	2.2	4.8	0.8	0.8	0.6	60.1	86.3	4.7	5.9	0.5	0.6	0.4	0.9	0.4	0.5	12.748
205654_at	NM_000715.4	complement component 4-binding protein, alpha	0.5	1.1	1.3	0.7	0.7	1.5	1.0	1.3	1.3	1.4	2.1	20.7	43.6	33.7	1.2	0.3	1.3	1.2	1.2	0.9	12.161
210773_s_at	U81501.1	formyl peptide receptor 2	0.8	0.1	0.6	0.6	0.3	0.6	0.6	0.6	0.6	0.5	86.9	105.0	50.2	59.9	0.1	1.0	0.6	6.0	0.8	0.1	12.14
206222_at	NM_03841.1	decoy receptor 1, TRAILR3	1.5	0.8	1.9	0.7	0.7	3.6	13.7	3.4	3.4	3.9	121.0	137.1	37.5	22.5	0.0	0.1	0.1	1.8	0.5	0.7	12.034
202083_s_at	NM_003003.1	SEC14 (S. cerevisiae-like)	0.8	0.2	0.9	1.8	3.0	2.2	2.6	3.8	3.8	2.6	36.7	25.9	33.9	32.6	1.3	0.1	0.1	1.1	1.0	0.7	11.729
211163_s_at	AF012536.1	R	0.2	0.1	2.2	1.5	0.6	2.6	12.3	9.4	9.4	6.4	87.9	110.9	60.4	55.8	0.5	0.2	0.1	0.7	0.1	0.6	11.404
205931_s_at	NM_004904.1	decoy receptor 1, TRAILR3 cAMP response element-binding protein CRE-BPa	0.0	0.1	0.3	0.1	0.6	0.6	0.6	0.6	0.6	0.7	23.2	14.5	20.5	12.9	1.6	0.8	0.1	1.6	0.1	0.1	10.618
205922_at	NM_004665.1	vanin 2	0.1	0.0	1.2	2.6	3.9	1.0	0.2	1.9	1.9	0.3	114.5	114.6	174.1	189.2	0.1	1.4	4.0	13.8	1.7	0.0	10.451
210176_at	AL050262.1	Toll-like receptor 1	0.7	0.6	0.2	0.3	0.3	0.5	1.1	1.9	1.9	1.2	29.5	38.6	25.1	32.6	1.6	0.8	0.7	3.0	1.5	0.3	10.418
215977_x_at	X68285.1	glycerol kinase	1.9	0.9	0.8	0.7	1.0	0.3	0.6	0.9	0.9	1.0	15.8	19.8	9.7	10.9	0.1	0.1	0.2	0.2	0.2	0.3	10.203
215783_s_at	X14174.1	liver-type alkaline phosphatase	0.5	1.2	0.7	0.9	0.4	0.7	0.5	1.0	1.0	0.6	21.2	42.8	11.6	12.8	1.2	0.7	0.2	0.5	0.5	0.5	10.167
217167_x_at	AJ252550	GK gene for glycerol kinase exon 1	1.2	0.1	0.2	0.3	1.0	0.2	0.1	0.8	0.8	0.3	8.0	13.6	7.5	7.2	0.4	0.1	0.1	0.9	0.2	0.2	10.067
213349_at	A094439	KIAA0779	0.9	0.7	0.9	1.4	1.0	1.9	1.4	2.3	2.3	2.1	15.6	15.3	19.5	23.8	0.1	1.4	1.4	1.5	1.2	1.2	9.7704

Fig. 6D

23/36

C. Neutrophil (Ne)-selective transcripts (2/7).

MC	cord blood	Transcripts	Accession #	Probe set	MC																				
					MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo	Eo (small)	Eo3 (small)	Eo4 (small)	Ne	Ne (small)	Ne3 (small)	Ne4 (small)	pI	CD4	CD8	CD14	CD19	Fb	Ne.S1		
GPR	1.1	0.4	1.9	1.4	1.5	2.0	1.5	2.5	0.4	19.4	18.6	22.6	15.5	0.7	1.6	0.9	2.0	0.3	1.1	9.2749					
	0.1	0.2	0.4	0.7	0.7	0.7	0.3	0.8	0.7	51.4	67.7	44.8	46.4	0.5	0.5	0.5	5.6	0.1	0.1	9.2661					
	0.7	0.5	1.6	0.2	0.5	1.1	0.9	0.7	0.5	26.3	20.5	6.6	2.8	0.2	0.7	0.4	1.1	0.2	0.4	9.1536					
	0.7	0.2	1.2	0.7	0.6	0.7	0.8	0.0	0.7	230.7	278.8	47.6	45.9	4.2	1.9	6.9	12.0	3.9	0.1	9.0769					
R	4.3	2.6	5.1	11.5	19.4	5.3	5.1	5.9	3.7	93.8	127.8	92.8	69.1	0.7	1.0	1.1	8.3	0.9	1.7	8.9855					
	0.1	0.0	1.3	0.7	0.8	0.7	0.2	2.0	1.4	7.9	8.4	7.9	8.9	0.3	0.1	0.0	1.7	0.1	0.0	8.866					
	1.1	0.8	3.2	4.0	2.9	2.8	2.8	4.7	3.2	24.7	25.2	33.2	29.3	0.1	1.5	1.2	1.7	2.0	2.6	8.3788					
	1.0	0.4	2.5	4.4	4.4	2.4	4.7	6.1	8.0	25.8	36.2	52.4	48.3	0.4	0.2	0.5	1.5	0.7	1.1	8.108					
ICN	0.0	0.1	0.9	2.0	1.6	0.8	0.6	2.3	2.7	7.9	5.9	20.1	18.0	0.2	0.5	0.2	0.1	0.2	1.2	7.9705					
	0.1	1.5	0.3	0.4	0.5	1.1	1.0	0.5	0.4	7.9	10.7	10.1	4.4	0.1	0.4	0.3	1.0	0.4	0.9	7.8712					
	0.0	0.0	0.8	1.8	1.0	3.0	5.4	11.7	9.4	46.0	51.5	56.9	43.0	0.1	0.0	0.0	0.6	0.6	0.1	7.5773					
	1.9	1.0	1.7	2.1	3.3	8.1	16.1	2.8	4.2	70.9	95.6	42.8	30.5	0.3	0.2	0.1	7.2	2.3	0.2	7.5239					
R	0.1	0.2	1.3	6.1	5.0	0.2	0.1	0.5	0.4	26.8	22.1	20.0	36.8	0.8	0.2	0.1	3.0	0.1	0.1	7.5216					
	5.6	4.4	4.8	6.5	9.6	7.6	6.8	5.3	7.3	109.5	89.0	52.9	61.4	2.5	4.9	7.0	10.0	3.9	6.5	7.5056					
	2.1	1.5	1.0	1.5	1.6	1.1	1.4	1.6	1.4	14.3	20.3	10.7	10.3	0.9	0.6	0.3	1.7	0.6	0.6	7.4603					
	1.1	0.2	0.8	0.6	0.9	5.9	8.3	2.1	4.1	46.3	41.2	25.1	25.8	0.4	0.9	0.6	3.7	1.6	0.5	7.4139					
	0.4	0.0	0.4	0.7	0.9	0.7	0.0	0.4	0.3	30.1	47.7	36.4	24.7	0.7	0.6	0.0	4.6	0.1	1.5	7.3246					
	1.3	0.3	0.4	0.2	0.5	2.9	0.7	1.4	1.5	92.8	84.0	81.2	98.6	3.4	0.6	0.1	12.3	0.9	0.3	7.2368					
	1.7	0.1	0.4	0.4	0.4	0.2	1.0	1.4	1.1	16.8	13.0	13.4	1.3	0.7	0.6	0.4	1.1	0.4	0.2	7.1328					
	0.5	0.1	0.1	0.4	0.1	0.1	0.0	1.1	0.0	3.4	4.1	4.3	0.7	0.1	0.3	0.1	0.4	0.0	0.2	7.0823					
	0.2	0.4	0.1	1.2	1.7	0.8	1.1	0.6	1.2	7.8	14.2	24.0	12.1	0.9	0.0	0.1	1.9	1.0	0.3	6.966					
	2.9	1.0	0.9	1.5	0.8	0.9	0.4	1.3	1.1	47.2	54.4	91.9	94.0	1.7	0.7	0.4	9.9	1.5	0.3	6.9074					
	1.2	1.4	3.5	5.9	5.1	6.5	5.1	8.5	7.1	43.7	40.6	45.2	56.0	0.7	1.3	2.9	5.1	0.8	1.2	6.8934					
	1.7	0.8	4.6	1.5	1.1	1.2	2.2	8.5	0.8	16.2	19.8	13.9	8.7	1.8	0.6	1.2	1.7	1.1	2.1	6.7497					
	2.0	0.9	0.4	0.6	1.0	0.7	0.6	0.5	1.0	10.3	18.6	5.8	5.8	0.5	0.2	0.2	0.8	0.3	0.1	6.6675					
	0.6	0.4	0.2	0.2	0.4	0.1	0.3	0.7	0.5	2.8	3.8	3.3	2.7	0.3	0.4	0.0	0.1	0.1	0.2	6.5382					
	0.3	0.6	0.1	0.1	0.1	0.3	0.8	0.4	0.3	8.9	7.2	9.1	7.0	1.2	0.6	0.0	0.1	0.1	0.2	6.4857					
	0.8	0.8	1.3	0.9	0.5	8.0	8.5	18.7	10.1	118.0	52.0	39.6	92.5	1.7	0.8	0.1	6.0	0.2	3.4	6.4779					
	2.2	2.6	1.3	0.7	0.5	1.6	0.6	0.5	1.0	22.6	25.0	11.3	8.3	1.3	1.2	1.5	1.8	1.5	0.9	6.4334					
	1.4	1.5	0.5	1.3	2.3	1.1	1.0	2.2	1.9	17.9	15.9	15.1	12.8	2.4	0.8	1.1	1.3	1.2	0.5	6.4271					
	0.7	0.0	0.1	2.6	2.1	1.8	1.5	2.4	2.0	10.3	11.2	15.4	12.8	1.9	0.1	0.5	0.2	0.1	0.5	6.3478					
	0.1	0.0	1.0	0.1	0.2	2.3	0.6	2.4	1.0	220.3	187.2	134.9	112.1	0.2	0.8	0.2	25.5	0.1	0.2	6.2051					
	0.9	1.1	1.6	1.8	1.9	1.1	1.9	1.7	2.0	11.1	7.0	13.7	14.1	1.4	1.3	0.9	1.6	1.1	0.6	6.172					
	1.5	1.2	1.2	1.2	1.8	3.3	3.2	2.6	1.8	25.2	23.3	17.9	21.8	0.5	0.6	0.4	3.6	0.4	0.6	6.112					
	4.7	1.2	0.9	1.2	2.4	1.9	22.8	19.4	21.4	104.3	129.0	153.0	123.9	4.0	0.7	0.7	16.3	2.2	0.2	6.1015					
	1.3	1.1	1.2	1.8	2.2	1.4	1.3	3.2	2.4	20.5	44.6	35.8	42.2	5.6	0.8	0.7	2.0	0.7	1.1	6.0724					

Fig. 6E

24/36

C. Neutrophil (Ne)-selective transcripts (3/7).

C. Neutrophil (Ne)-selective transcripts (3/7).																						
Probe set	Accession #	Transcripts	MC cord	MC blood	Ba1 (small)	Ba2 (small)	Ba3 (small)	Bo 1	Bo 2	Bo 3	Bo 4	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne.SI.
207624_s_at	NM_000328.1	retinitis pigmentosa GTPase	0.0	0.6	1.1	2.0	1.2	1.1	1.2	2.1	2.8	7.1	7.0	13.6	15.1	0.2	1.2	0.4	0.9	0.7	0.3	6.0348
209850_s_at	BC005406.1	regulator (RGR)	0.2	0.2	1.3	0.2	1.0	0.2	0.4	0.5	0.4	13.2	9.6	6.7	8.7	0.2	0.2	0.2	0.6	0.4	1.6	5.9313
209396_s_at	NM_004994.1	Cdc42 effector protein 2	4.7	0.6	1.6	1.9	1.4	1.2	2.4	15.5	1.5	36.5	35.1	36.8	21.9	1.7	2.0	1.4	1.9	1.3	1.4	5.9311
215966_x_at	AA292874	matrix metalloproteinase 9 glycerol kinase	1.2	0.2	0.6	0.1	1.2	0.2	1.0	1.2	1.2	6.6	10.2	7.3	7.4	0.2	0.1	0.2	1.3	0.5	0.0	5.9077
206925_at	NM_005668.1	sialyltransferase 8	3.1	1.2	2.1	2.5	2.0	1.4	3.1	1.6	1.6	21.7	33.3	6.8	11.4	0.4	0.9	1.6	2.6	1.2	0.2	5.8688
211764_s_at	BC005980.1	ubiquitin-conjugating enzyme E2D 1	1.8	1.4	1.1	2.9	2.4	7.5	5.7	3.9	2.2	29.3	31.2	52.6	25.4	0.2	2.0	1.4	5.7	1.3	2.3	5.8143
201192_s_at	NM_006224.1	phosphotyrosyl transfer protein (PTPN)	3.0	3.1	1.9	5.0	4.6	3.9	5.4	6.6	5.4	27.9	26.9	32.9	35.2	2.0	3.5	3.7	5.0	3.2	2.8	5.811
205921_s_at	U16120.1	ubiquitin c-terminal hydrolase	1.2	0.7	0.5	0.2	0.4	0.3	1.6	0.5	0.9	14.8	17.2	2.8	2.6	0.0	0.1	0.3	1.1	0.3	0.4	5.7909
209137_s_at	BC000263.1	placental taurine transporter related polypeptide	3.6	4.1	2.0	2.6	1.9	1.5	0.9	2.7	0.9	25.0	24.5	37.6	29.7	3.5	5.0	2.5	3.5	2.7	3.0	5.7864
208052_x_at	NM_001815.1	carcinoembryonic antigen-related cell	1.7	1.4	2.9	2.7	1.9	3.0	2.6	2.8	2.1	14.3	16.5	20.0	13.7	2.5	1.3	2.3	2.8	2.5	1.6	5.7572
201393_s_at	NM_000876.1	adhesion molecule 3 (CEACAM3)	6.4	2.8	0.2	0.8	1.8	4.1	5.4	6.8	5.4	82.4	106.9	80.1	71.7	1.7	2.9	8.7	8.4	4.8	14.8	5.7104
218614_at	NM_018169.1	insulin-like growth factor 2 receptor	1.2	1.0	6.9	13.7	12.5	3.2	3.3	7.7	5.8	52.7	54.4	82.8	83.3	2.9	8.7	11.8	3.2	10.8	1.3	5.6442
202084_s_at	NM_003003.1	FLJ10652	5.7	2.5	12.8	28.8	22.6	20.6	18.7	35.5	29.5	130.7	129.7	135.6	177.9	19.2	4.1	3.5	11.5	7.7	11.8	5.6423
32069_at	AB014515	SEC14 (S. cerevisiae)-like 1 KIAA0615	2.8	1.5	2.1	5.6	5.5	4.6	3.7	5.9	6.9	23.9	20.9	35.1	40.5	1.0	3.4	3.3	2.6	2.1	1.5	5.6348
205896_at	NM_003059.1	solute carrier family 22, member 4 (SLC22A4)	0.8	1.2	1.0	0.1	1.1	1.9	2.4	3.5	2.7	8.5	13.3	30.0	12.6	0.5	0.7	0.8	2.6	0.5	1.4	5.4612
206584_at	NM_015364.1	MD-2 protein	7.4	1.7	2.0	3.9	1.8	1.0	0.4	0.6	0.5	43.9	62.3	87.8	56.0	1.3	3.5	1.0	11.1	3.5	9.4	5.4459
202082_s_at	NM_003003.1	SEC14 (S. cerevisiae)-like 1	1.0	0.3	3.6	2.5	2.2	15.5	5.4	12.3	8.4	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	3.3	2.4	5.4422
204308_s_at	NM_014844.1	KIAA0329	2.9	1.7	2.2	2.8	2.8	2.1	3.1	3.1	4.3	16.5	18.7	19.9	19.0	3.4	1.3	1.7	1.8	1.3	2.5	5.4369
207500_at	NM_004347.1	caspase 5	0.3	1.1	0.1	0.0	0.1	0.1	0.3	0.2	0.5	4.2	6.2	4.6	2.9	0.3	0.3	0.4	0.8	0.1	0.3	5.379
203435_s_at	NM_007287.7	CD10, membrane metallo-endopeptidase	0.3	0.5	0.4	0.3	0.2	0.1	0.3	0.3	0.2	16.4	44.2	54.6	42.8	0.2	0.3	0.2	0.2	0.2	6.9	5.2591
205539_at	NM_006576.1	adiponin	0.4	0.5	2.0	1.4	0.8	1.0	1.1	1.0	1.1	8.4	6.9	6.0	10.1	1.0	1.3	0.4	1.5	0.7	1.1	5.2541
204601_at	NM_014664.1	KIAA0615	1.9	1.2	1.3	3.2	2.3	3.0	2.7	3.7	3.0	12.9	12.8	20.2	20.0	0.1	2.2	2.6	1.3	1.9	1.0	5.2381
201963_at	NM_021122.2	fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)	2.9	2.1	5.0	19.9	33.4	6.6	3.8	10.3	6.1	58.8	86.6	92.2	80.2	0.1	1.1	1.1	1.1	1.5	2.4	5.2374
207064_s_at	NM_009590.1	CXCR1, interleukin 8 receptor, alpha	0.7	0.1	0.9	0.9	0.8	0.8	0.8	0.9	1.2	4.3	4.7	4.0	6.6	0.8	0.5	0.8	0.5	0.8	0.3	5.1905
220005_at	NM_023914.1	P2YX purinergic receptor GPR86 for UDP-glucose	0.6	0.0	0.1	0.5	0.1	19.7	9.6	25.1	17.3	76.5	77.1	100.7	98.6	1.9	0.1	0.2	12.3	0.6	0.0	5.1686
211395_x_at	U90940.1	Fc gamma receptor IIc3	4.6	0.3	7.3	9.7	15.1	9.7	19.5	4.4	6.6	115.0	140.3	42.9	38.9	3.0	1.4	0.6	14.0	7.2	1.0	5.1401
201780_s_at	NM_007282.1	ring finger protein 13 (RNF13)	4.4	2.8	3.5	9.2	6.6	6.8	6.2	8.9	7.1	27.1	36.6	52.5	35.7	0.8	4.1	3.7	7.2	7.2	4.6	5.1305
209864_at	AB045118.1	GSK-3 binding protein FRAT2	2.8	1.3	4.4	9.2	8.0	13.4	16.9	27.3	22.6	93.2	97.2	100.6	104.2	1.3	1.9	2.9	10.2	2.5	1.0	5.1047
218319_at	NM_020651.2	pellino (Drosophila) homolog 1 (PELI1)	3.4	2.9	5.9	17.5	33.5	17.7	11.7	12.6	15.1	64.9	88.3	73.0	80.2	2.4	6.3	2.9	13.8	12.6	1.1	5.0403
206632_s_at	NM_004900.1	phorbol	0.6	1.1	1.0	1.2	2.6	1.3	0.8	3.9	0.5	19.6	11.1	30.8	0.5	1.5	0.2	0.4	0.4	1.0	1.2	5.0277
220990_s_at	NM_030938.1	DKFZp5661133	11.7	6.2	4.6	18.5	12.5	5.0	3.3	8.2	4.9	115.5	117.2	125.3	122.5	2.6	5.3	4.2	24.1	4.4	8.3	4.9558
221653_x_at	BC004395.1	apolipoprotein L1	0.7	2.8	0.6	2.1	1.6	2.0	0.4	1.8	1.1	8.0	3.9	12.7	5.2	0.2	0.9	0.4	1.4	1.1	0.4	4.9332
204748_at	NM_00963.1	COX2 prostaglandin-endoperoxide synthase 2	6.5	16.2	0.6	2.4	2.0	4.5	2.3	3.4	3.4	35.8	44.1	44.6	91.8	0.4	0.6	0.2	4.3	0.3	0.5	4.9206
210423_s_at	L32185.1	integral membrane protein	2.0	0.2	1.4	1.6	1.3	1.3	2.2	1.5	2.0	85.0	78.5	75.2	52.9	1.9	0.4	1.9	14.7	1.0	1.0	4.8845
206429_at	NM_005242.2	PAR2, protease activated receptor-2	0.8	0.8	0.9	0.9	0.2	0.9	0.9	0.2	0.8	11.8	15.1	4.1	4.1	1.3	1.5	0.2	1.5	0.3	0.7	4.8608
213352_at	A934469	KIAA0779	0.6	0.9	1.2	1.5	1.2	1.2	1.5	1.5	2.2	8.4	6.0	8.7	7.7	1.6	0.9	1.5	1.0	1.3	0.8	4.8373
201888_s_at	U81379.3	interleukin-13 receptor	0.1	0.6	0.3	0.2	0.0	1.7	2.7	1.7	2.0	8.6	19.0	15.0	13.9	0.4	0.4	0.4	0.3	1.3	1.3	4.746

Fig. 6F

25/36

C. Neutrophil (Ne)-selective transcripts (4/7).

Probe set	Accession #	R	Transcripts	MC	MC	Ba1	Ba2	Ba3	EO	EO	EO3	EO4	Ne	Ne	Ne3	Ne4	p1	CD4	CD8	CD14	CD19	Fb	BaSL
204780_s_at	AI164751		CD95, Fas, APO-1	1.4	1.4	7.2	14.0	11.5	6.6	6.7	9.3	6.6	4.53	388	65.5	51.8	2.6	5.6	4.8	3.6	2.6	9.7	4.7254
209310_s_at	U25804.1		Ich-2 cysteine protease	2.5	1.9	2.1	7.7	7.0	1.4	1.3	1.3	1.4	19.1	17.5	36.7	23.5	2.9	4.1	4.5	4.9	3.9	2.2	4.6817
205452_at	NM_004855.1		phosphatidylinositol glycan, class B (PIGB)	2.3	2.7	2.3	6.4	7.7	2.3	1.4	3.0	3.0	16.3	17.6	22.2	39.3	1.7	2.0	2.9	2.8	3.5	2.2	4.6577
218298_s_at	NM_024952.1		FLJ20950	3.1	3.3	5.4	8.1	7.2	5.7	5.7	8.8	9.4	37.2	23.4	37.3	39.1	0.6	1.7	3.1	5.8	2.3	2.7	4.6558
221210_s_at	NM_030769.1		swine acylneuraminase lyase	3.8	1.2	0.8	1.2	1.4	3.0	4.7	3.2	4.6	20.4	23.6	23.5	18.3	0.6	0.1	0.3	4.6	0.5	0.1	4.6378
221497_x_at	BC005359.1		chromosome 1 open reading frame	3.0	2.4	4.3	5.7	5.9	3.3	7.6	7.9	5.4	29.3	32.4	24.3	21.5	1.8	3.1	2.9	2.9	1.9	2.0	4.6333
204668_at	AL031670		12, clone MGC12484	0.8	0.5	1.8	1.0	1.2	0.3	1.5	1.7	0.9	8.4	8.1	7.0	6.5	1.4	1.3	1.0	1.5	0.5	1.6	4.614
201921_at	NM_004125.1		ferritin, light polypeptide-like 1	7.1	5.4	2.6	6.7	6.5	11.7	11.4	20.8	15.3	45.5	87.5	81.3	57.1	0.8	2.7	3.0	8.4	3.2	12.4	4.5644
209600_s_at	S69189.1		guanine nucleotide binding protein 10 (GNG10)	2.9	1.7	2.8	5.3	4.7	1.4	1.0	1.2	1.3	15.0	17.7	21.4	21.2	0.4	1.0	0.8	2.1	0.7	1.5	4.5552
205119_s_at	NM_020292.1		peroxisomal acyl-coenzyme A oxidase	4.1	1.4	11.2	26.6	32.7	14.0	11.1	4.2	6.0	28.2	31.58	274.7	252.9	3.6	1.3	0.7	6.26	1.1	0.5	4.505
217738_at	BF575514		formyl peptide receptor 1	5.7	0.9	7.4	24.1	34.9	7.5	4.6	5.1	3.9	73.4	87.0	89.9	79.9	2.2	1.7	1.6	10.1	1.7	2.8	4.4839
215078_at	AL050388.1		pre-B-cell colony-enhancing factor	0.0	0.1	0.0	0.1	0.4	0.9	0.5	0.8	0.3	7.1	12.9	4.5	7.9	0.1	0.5	0.5	1.7	0.1	0.1	4.4343
207545_s_at	NM_033744.1		DKE2p564M2422	0.0	0.7	1.4	1.1	2.5	2.4	1.8	2.9	1.2	7.2	11.2	10.5	7.4	0.8	0.5	0.5	1.6	1.1	1.2	4.3728
213418_at	NM_002155.1		numb (Drosophila) homolog	1.1	0.4	0.7	1.5	1.6	2.53	2.88	10.5	17.0	104.0	91.6	70.0	70.8	0.5	1.1	1.1	12.8	4.7	0.5	4.3655
218023_s_at	NM_016605.1		heat shock 70kD protein 6 (HSP70B)	5.7	3.8	6.6	13.0	12.6	8.5	10.3	13.0	10.9	40.1	39.7	47.0	59.7	3.0	4.4	5.9	7.0	6.0	6.8	4.3383
210366_s_at	BC001906.1		putative nuclear protein (LOC51307)	6.2	1.9	2.7	5.4	4.0	1.4	2.2	1.8	3.6	19.5	15.8	23.4	23.8	2.5	3.6	2.6	4.1	2.6	4.7	4.3318
207643_s_at	NM_001065.1		Similar to metaxin 1	1.8	1.6	0.9	1.3	1.4	6.3	7.4	8.5	9.0	81.1	83.6	68.6	65.6	1.3	2.2	5.9	17.4	0.6	16.0	4.2796
203140_at	NM_001706.1		CD120a, TNF-R1 p55	6.2	2.9	9.1	13.5	19.8	23.5	16.7	28.7	33.1	99.1	107.8	115.8	101.1	2.2	3.4	3.4	23.4	6.7	6.5	4.2767
207253_s_at	NM_016936.1		B-cell lymphoma 6 (BCL6)	3.2	2.8	2.9	4.4	5.0	3.8	2.6	3.8	3.6	16.7	20.0	14.2	17.8	2.3	2.5	2.5	2.2	2.4	1.8	4.2556
202875_s_at	BE397715		ubiquitin 1	2.0	1.4	0.1	0.1	0.2	2.5	3.6	2.1	1.5	11.6	15.4	6.8	7.5	0.8	1.7	1.9	1.1	1.3	0.7	4.2425
218791_s_at	NM_024713.1		pre-B-cell leukemia transcription factor 2	1.2	0.7	2.5	2.7	1.8	0.9	1.5	1.6	7.0	6.9	8.7	13.2	11.2	1.4	1.0	0.5	1.3	0.8	1.2	4.2114
211862_x_at	AF015451.1		FLJ2257	3.5	2.6	16.8	9.7	10.1	5.6	10.2	7.7	1.0	65.7	67.7	36.1	37.9	3.1	6.8	8.7	10.1	6.9	2.0	4.2001
217986_s_at	NM_013448.1		Usurin-beta	3.5	3.0	3.5	9.2	8.4	6.1	8.5	14.5	13.1	39.0	35.1	43.5	51.6	2.5	5.9	6.5	7.0	5.0	1.7	4.1976
217966_s_at	NM_022083.1		bromodomain adjacent to zinc finger domain, 1A	4.1	1.9	6.4	7.4	9.0	24.2	14.8	25.6	11.8	51.9	105.3	76.2	80.0	0.9	3.3	3.8	3.2	2.0	8.2	4.1858
212602_at	AB06395		nidogen	2.3	3.5	0.4	0.9	1.1	0.8	0.6	0.4	0.8	17.1	18.1	12.9	13.4	1.5	0.5	0.3	3.6	0.8	2.8	4.1806
208485_x_at	NM_003879.1		CASP8 and FADD-like apoptosis regulator (CFAR)	3.2	2.5	19.2	9.8	9.9	6.2	13.0	8.1	8.3	70.8	69.7	33.8	41.4	3.5	6.4	8.4	11.5	6.6	2.0	4.1719
201942_s_at	D85390.1		gp 180-carboxypeptidase D-like enzyme	0.6	1.7	0.6	1.3	1.7	1.6	7.0	2.4	2.6	15.9	23.8	6.8	8.1	0.5	0.8	1.3	2.5	0.5	2.6	4.1525
220933_s_at	NM_024617.1		FLJ13409	2.1	2.0	9.6	14.2	14.0	7.1	7.2	10.9	12.5	38.1	37.3	81.5	57.8	1.9	3.1	4.8	6.2	3.8	3.0	4.1025
221764_at	AL574186		glycerol-3-phosphate dehydrogenase	6.3	4.4	16.5	18.6	15.0	10.4	15.8	21.9	22.7	80.9	99.2	46.3	60.3	9.5	8.9	9.4	5.7	9.4	2.5	4.0745
207446_at	NM_006068.1		Toll-like receptor 6	0.5	0.5	0.7	1.5	0.8	0.8	0.9	1.2	0.8	7.6	11.8	7.2	8.7	0.1	0.9	0.9	2.1	1.2	0.6	4.0697
219748_at	NM_024807.1		chromosome 6 open reading frame 76	0.2	0.3	0.3	0.4	0.6	1.9	2.6	1.6	1.6	9.1	9.1	6.7	6.4	0.2	0.3	0.6	0.5	1.1	0.0	4.0619
220945_x_at	NM_018050.1		FLJ10298	1.0	1.4	0.5	0.7	0.7	1.1	0.6	1.5	1.0	8.0	10.8	13.6	11.0	1.1	0.5	0.3	0.9	0.6	2.6	4.057
212577_at	AA869754		KJAA0650	1.9	1.3	6.4	8.0	9.9	10.1	24.0	8.1	9.4	74.0	98.6	42.2	57.4	4.4	10.8	9.5	7.5	16.0	3.2	4.0417
221732_at	AK026161.1		RIKEN cDNA 5830420C20	2.8	0.7	3.4	10.5	8.8	5.0	6.0	10.7	10.9	27.6	31.6	30.8	34.7	0.3	0.4	1.8	2.5	1.6	4.6	4.041
205986_at	NM_004920.1		apoptosis-associated tyrosine kinase	1.6	1.3	0.7	1.0	0.5	0.3	0.3	1.4	1.0	10.5	15.8	13.3	15.2	3.2	1.0	0.5	3.4	0.9	0.4	4.0322
213501_at	T62985		acyl-Coenzyme A oxidase 1, palmitoyl	1.3	1.1	2.0	2.6	2.8	1.3	0.9	1.2	0.6	8.5	11.5	12.4	7.5	0.1	1.1	0.3	1.8	0.5	1.1	4.0194
204542_at	NM_006456.1		salt/transferase (STHM)	0.4	0.2	1.5	0.3	0.2	3.4	3.9	4.5	3.2	13.0	13.4	21.0	13.4	0.7	0.7	0.3	1.4	0.3	0.6	4.016

Fig. 6G

26/36

C. Neutrophil (Ne)-selective transcripts (5/7).

MC		cord blood		Transcripts		MC	Ba.1	Ba.2	Ba.3	EO	EO3	EO4	Ne	Ne2	Ne3	Ne4	p1	CD4	CD8	CD14	CD19	Fb	Ne.S1
Probe set	Accession #																						
204071_s_at	NM_005802.1	tumor protein p53-binding protein	1.4	1.6	1.1	3.0	2.9	3.7	2.3	2.6	2.6	2.2	10.5	12.8	8.0	11.9	1.5	2.2	2.2	1.4	2.2	2.1	4.0148
210594_x_at	AF239756.1	myelin protein zero-like 1	1.2	0.5	0.6	1.5	1.2	0.1	0.4	0.8	0.8	1.9	15.3	13.9	7.1	10.9	0.3	0.2	0.6	1.0	0.7	2.8	3.9778
R	203063_at	protein phosphatase 1F (PP2C domain containing)	0.5	0.4	1.4	3.3	3.0	4.0	6.0	6.1	10.0	33.1	22.2	29.6	31.8	0.3	2.9	1.2	7.3	1.5	1.8	3.9764	
	201992_s_at	insulin-like growth factor 2 receptor	1.7	0.7	0.1	0.0	0.1	2.6	3.0	1.9	1.5	51.1	59.1	12.8	15.0	1.1	1.2	4.0	3.8	2.2	7.0	3.9602	
	221477_s_at	MGC5618	2.9	1.4	3.4	4.3	9.0	4.2	4.2	4.2	4.2	56.8	63.6	36.1	46.6	7.9	3.2	1.2	12.6	2.7	2.1	3.9562	
R	206756_at	carbohydrate (N-acetylglucosamine 6-O-sulfotransferase 7	0.2	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.1	0.1	5.0	3.9	3.5	10.5	0.1	1.3	1.0	1.0	0.2	0.5	3.9516
	204994_at	myxovirus (influenza) resistance 2 (MX2)	1.3	2.3	5.4	7.8	8.2	9.2	11.6	15.2	12.3	49.8	46.6	77.6	80.8	2.4	7.5	6.0	15.6	4.8	1.8	3.9478	
	201943_s_at	carboxypeptidase D	0.9	0.9	0.5	2.1	3.6	1.7	7.6	7.2	4.6	16.4	21.3	18.7	15.2	0.7	1.0	1.7	3.3	0.4	3.8	3.8926	
R	216252_x_at	CD95, Fas, APO-1	0.3	0.8	4.3	2.5	1.1	1.8	4.7	1.8	1.7	18.5	31.2	10.3	8.4	2.2	3.8	2.4	1.9	1.4	3.9	3.8691	
	203066_at	B cell RAG associated protein (BRAG)	1.3	3.9	0.9	1.2	1.0	10.6	10.2	13.1	20.2	57.0	65.9	95.2	86.9	1.9	0.1	0.0	19.3	4.2	5.9	3.8667	
	212479_s_at	FLJ13910	1.7	1.6	2.1	2.5	2.6	2.4	2.5	3.5	1.7	9.0	10.1	8.8	9.8	1.1	2.3	2.4	2.2	1.9	0.9	3.8422	
R	209571_at	receptor	0.7	0.2	1.6	3.3	2.7	2.2	1.3	2.6	2.7	6.8	7.8	12.8	10.9	0.8	1.0	1.1	1.2	1.5	1.1	3.8367	
	211317_s_at	CASP8 and FADD-like apoptosis regulator	1.6	1.8	9.5	3.6	4.0	3.7	6.8	3.2	2.8	33.1	44.8	15.2	17.6	2.4	4.7	6.5	5.7	4.9	1.1	3.8332	
	209732_at	C-type (calcium dependent, carbohydrate-recognition domain)	8.1	5.9	10.0	18.6	23.6	9.0	10.0	8.9	7.3	72.9	77.0	99.7	75.5	4.1	14.4	21.2	10.2	16.4	1.3	3.8003	
R	201779_s_at	lectin, superfamily member 2	14.8	5.9	13.0	13.3	13.9	21.8	27.0	25.3	13.1	88.2	108.1	116.5	81.8	6.0	9.6	11.3	25.7	15.7	8.5	3.7993	
	212441_at	clone 24450 RING zinc finger protein RZF	5.4	2.9	3.5	9.8	10.3	8.0	6.9	11.5	11.3	31.9	30.1	30.8	49.8	2.5	2.0	4.0	5.9	2.1	4.9	3.7868	
	205920_at	KIAA0232	1.2	1.4	0.9	0.2	0.2	1.1	5.2	0.7	1.4	33.1	26.7	2.7	4.0	0.3	0.1	0.4	2.6	0.1	0.5	3.7836	
R	213596_at	solute carrier family 6, member 6 (SLC6A6)	0.7	0.7	2.3	3.6	3.0	1.2	1.2	1.1	1.2	10.6	10.9	12.5	9.9	2.2	1.1	2.0	1.5	0.7	0.3	3.7615	
	209508_x_at	DKFZ586A181	1.7	2.7	10.8	7.6	11.5	4.9	6.3	6.0	8.4	37.0	34.8	34.7	40.8	2.7	4.0	5.1	6.3	3.4	1.3	3.7451	
	218115_at	caspase-like apoptosis regulatory protein (clarp)	0.9	2.2	2.4	1.5	0.9	1.8	2.1	1.3	1.3	1.1	10.5	9.1	6.7	7.7	1.1	1.2	2.2	2.1	1.7	1.5	3.7435
R	215652_at	FLJ10604	0.2	0.1	2.0	0.3	1.6	0.3	0.3	1.2	0.7	5.5	4.5	3.4	2.5	0.1	0.3	1.0	0.9	0.2	0.6	3.7249	
	212561_at	FLJ14320	10.0	6.1	10.2	12.4	11.4	18.7	14.9	12.1	10.0	66.3	60.0	47.6	37.1	4.0	8.7	9.9	13.9	5.9	10.2	3.6962	
	204166_at	RAB6 interacting protein 1	3.6	0.4	1.1	0.0	0.1	1.0	1.3	0.1	0.8	11.8	12.5	4.0	2.9	0.3	0.9	1.7	1.7	1.2	0.2	3.6908	
R	221874_at	KIAA0963	0.3	0.3	0.7	1.1	0.3	0.8	0.8	0.7	0.5	9.1	5.1	5.1	1.2	0.9	1.1	0.7	0.5	0.6	0.4	3.6808	
	217207_s_at	KIAA1324	1.2	1.1	1.4	2.1	1.7	1.2	1.9	0.6	2.4	10.9	3.4	7.2	6.1	1.5	1.7	1.6	0.9	1.5	1.3	3.6795	
	212579_at	butyrophilin like receptor	1.3	1.6	5.3	9.8	15.5	7.3	7.8	11.3	8.3	32.8	42.9	40.0	39.7	2.0	5.4	5.7	3.1	10.5	2.2	3.6784	
R	212657_s_at	KIAA0650	48.8	2.3	0.9	0.5	0.6	2.1	0.9	1.5	1.3	35.2	37.0	48.2	35.5	0.6	0.8	0.3	9.3	0.4	0.6	3.6759	
	202392_s_at	IL-1 receptor antagonist IL-1Ra (IL-1RN)	3.4	2.7	6.2	11.7	6.8	3.4	4.7	5.4	4.7	32.8	31.0	22.0	32.3	0.8	1.6	1.4	4.2	1.4	1.2	3.6753	
	206177_s_at	phosphatidylserine decarboxylase arginase (ARG1)	0.5	1.3	2.2	0.4	0.6	0.9	0.8	7.2	0.7	3.9	4.3	8.1	5.0	1.1	0.1	0.4	0.6	0.7	0.0	3.6722	
R	200706_s_at	LPS-induced TNF-alpha factor (PIG7)	31.2	39.0	20.7	64.6	62.5	15.6	13.4	31.8	21.7	173.2	148.5	172.0	150.2	8.5	13.3	42.7	14.3	16.7	18.2	3.6696	
	212478_at	FLJ13910	0	0.1	0.2	2.3	3.5	1.4	0.8	1.5	1.0	3.7	3.0	4.8	6.5	0.1	0.3	1.1	0.6	0.4	0.5	3.6623	
	218660_at	cysteinyl	2.5	0.5	1.5	0.2	0.2	1.7	0.2	2.6	1.1	48.5	51.8	44.5	20.4	0.3	1.2	1.7	10.6	0.2	1.3	3.6616	
R	211982_x_at	exportin 6	9.8	6.7	14.9	31.8	27.8	24.6	24.0	34.0	24.0	107.2	101.1	86.6	90.2	6.6	17.5	17.4	9.6	11.5	7.7	3.6408	
	202748_at	guanylate binding protein 2, interferon-inducible (GBP2)	2.4	5.3	3.7	9.0	7.4	3.3	2.1	3.0	3.3	28.1	35.2	45.0	24.8	4.2	7.3	9.0	6.3	1.9	3.7	3.6111	
	220980_at	Csa receptor	2.2	2.3	15.4	24.6	24.8	17.1	15.6	9.8	12.0	90.5	104.5	84.4	91.1	2.3	1.2	0.5	25.6	1.0	0.4	3.6036	
R	202890_at	microtubule-associated protein 7	0.9	0.1	0.7	1.4	1.1	0.1	0.0	0.2	0.1	2.5	3.1	3.2	7.1	0.0	0.1	0.4	0.1	0.1	0.0	3.6032	
	220987_s_at	DKFZP434J037	1.4	0.3	3.9	4.9	4.7	9.6	9.3	14.1	11.7	43.0	35.6	57.8	57.6	5.3	4.7	4.8	11.1	13.3	2.0	3.5748	

Fig. 6H

27/36

C. Neutrophil (Ne)-selective transcripts (6/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	EO 1	EO 2	EO3 (small)	EO4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	p1	CD4	CD8	CD14	CD19	Fb	NeSL
207072_at	NM_003853.1	interleukin 18 receptor accessory protein (IL18RAP)	59	09	22	34	4.1	7.2	1.6	2.8	1.7	13.4	9.7	20.9	5.6	2.4	2.8	3.1	0.4	1.6	0.3	35722
215719_x_at	X83493.1	CD95, Fas, APO-1	1.0	0.6	3.1	2.7	1.6	2.2	5.2	1.8	1.7	19.0	31.9	11.4	9.4	1.0	4.5	2.2	1.6	1.1	4.4	35657
218404_at	NM_013322.1	sorting nexin 10	4.9	1.2	2.6	5.0	3.7	0.7	0.1	2.1	0.7	28.5	31.8	34.8	33.8	0.3	1.2	1.9	9.0	6.5	0.3	3563
219394_at	NM_024419.1	phosphatidylycerophosphate synthase (PGS1)	3.4	3.0	1.7	4.2	3.5	2.4	3.8	6.1	9.2	17.2	16.9	17.5	16.3	1.0	2.1	2.6	2.4	1.5	1.7	35544
216913_s_at	AK021460.1	KIAA0690	0.1	0.3	0.1	0.1	0.1	1.9	2.5	2.3	2.8	8.9	8.3	7.5	10.9	0.1	0.1	0.2	2.5	0.1	0.0	35402
205118_at	M60626.1	formylpeptide receptor 1	0.1	0.2	0.8	0.1	1.1	0.1	0.4	0.6	0.1	3.9	7.0	3.2	7.8	0.2	0.1	0.1	1.4	0.1	0.0	35295
210564_x_at	AF009619.1	FLAME-1-delta	1.4	1.5	5.3	6.6	7.0	4.3	4.2	5.9	3.5	21.2	30.3	18.4	19.6	2.1	2.9	4.0	4.6	3.0	1.8	35148
213607_x_at	BE551347	KIAA0134	1.3	1.3	2.9	2.0	1.7	8.7	15.8	3.5	4.3	42.7	42.5	11.1	15.3	0.6	1.3	1.9	6.2	1.7	0.9	3514
203888_at	NM_000361.1	thrombomodulin	0.9	0.6	0.1	0.1	0.3	0.2	0.4	0.8	0.1	6.1	6.4	4.6	0.2	0.3	0.3	0.1	0.6	0.5	0.1	35126
210233_at	AF167343.1	interleukin-1 receptor accessory protein (IL1RAP)	0.5	0.1	0.0	0.1	0.6	0.8	0.4	0.6	0.7	1.8	3.0	2.0	2.3	0.6	0.0	0.0	0.0	0.0	0.3	35023
204959_at	NM_002432.1	myeloid cell nuclear differentiation antigen	1.2	0.6	24.2	50.0	26.2	17.5	17.9	49.8	22.3	249.8	290.2	186.0	217.0	3.4	1.6	0.6	66.6	2.5	0.0	34903
217967_s_at	AF288391.1	niban	63	3.7	163	42.4	35.9	27.9	29.5	43.0	30.9	107.4	115.3	117.9	110.3	2.6	7.5	9.9	4.9	3.4	20.4	34847
221763_at	A1694023	thyroid hormone receptor interactor 8	0.8	1.5	1.9	4.6	5.5	5.5	6.9	9.9	9.0	28.3	32.9	34.0	42.7	1.1	3.7	4.1	5.1	9.8	3.0	34777
207857_at	NM_006866.1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain) member 2 (LILRA2)	0.4	0.5	3.6	8.5	5.3	4.5	4.9	1.6	6.3	33.5	34.3	46.2	50.8	1.8	0.0	0.1	11.6	0.5	0.1	34773
220740_s_at	NM_005135.1	solute carrier family 12 member 6 (SLC12A6)	1.6	1.0	2.5	3.3	3.4	3.5	5.6	3.2	3.2	12.6	19.0	10.7	14.4	4.0	2.9	2.2	2.9	3.5	0.8	34722
217739_s_at	NM_005746.1	p18-8 cell colony-enhancing factor	7.1	1.7	9.9	46.0	61.0	18.9	13.9	12.9	9.3	112.4	120.5	90.8	93.4	1.2	2.3	1.4	17.6	2.1	3.1	34242
205041_s_at	NM_000607.1	oroscuroid 1 (ORM1)	0.3	1.0	0.4	0.1	0.1	0.0	0.1	1.0	0.1	2.6	3.6	2.7	0.4	0.1	0.2	0.1	0.5	0.0	0.1	34189
214784_x_at	BE566299	exportin 6	7.4	5.0	10.0	23.7	23.9	13.0	16.7	23.3	20.5	60.3	67.8	57.2	60.8	2.9	8.7	7.8	6.6	5.9	5.4	34155
217985_s_at	AA102574	bromodomain adjacent to zinc finger domain, 1A	1.5	1.4	1.8	2.6	3.8	7.4	5.1	7.3	4.7	16.9	19.2	22.1	24.2	2.7	2.5	2.3	3.5	2.4	0.9	33999
212598_at	A1806395	KIAA0593	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	5.5	7.3	3.1	3.2	0.2	0.1	0.0	1.0	0.1	1.3	33933
219033_s_at	NM_017966.1	FLJ20847	2.6	2.0	1.9	2.3	2.3	2.6	2.1	3.0	2.8	11.3	7.6	22.2	34.1	1.6	0.5	0.9	4.7	1.3	2.9	33686
217475_s_at	AC002073	PAC clone RP3-515N1	0.6	0.5	0.6	0.2	0.4	1.3	1.3	0.5	1.2	5.9	9.8	1.6	1.4	0.7	0.3	0.1	0.5	0.7	0.2	33448
46323_at	AL120741	Ca2+-dependent endoplasmic reticulum nucleoside diphosphatase	4.4	3.2	4.2	8.3	7.2	5.3	6.7	11.4	7.9	20.0	21.5	33.9	26.3	2.5	2.8	3.6	4.3	3.4	5.0	33028
201965_s_at	NM_015046.1	KIAA0625	2.7	3.1	3.3	8.5	8.3	4.9	5.8	7.4	7.5	19.5	18.5	18.7	27.8	2.2	3.9	3.4	4.6	5.6	2.6	33019
203628_at	NM_000875.2	insulin-like growth factor 1 receptor	0.5	0.1	3.7	3.0	4.0	6.8	4.9	2.7	5.8	18.8	23.4	6.8	20.6	1.6	0.1	2.8	2.4	2.0	3.5	32989
202193_at	NM_005569.2	LIM domain kinase 2 (LIMK2)	1.8	1.5	1.9	5.6	5.6	6.4	4.8	11.3	8.9	17.0	20.5	36.5	28.2	0.1	1.3	1.1	0.6	0.5	0.8	32887
203042_at	NM_002294.1	transcript variant 2a	2.4	3.1	1.1	1.7	1.3	5.9	6.4	12.4	10.7	21.3	27.0	44.1	35.4	0.8	0.6	0.5	3.2	0.8	9.4	3282
220326_s_at	NM_018071.1	protein 2 (LANP2)	5.1	4.5	1.9	1.2	1.9	6.3	8.9	5.2	8.5	25.3	28.1	19.2	21.0	0.9	0.1	0.7	6.4	0.1	4.1	32759
212470_at	AB011088.1	FLJ10357	4.0	2.9	3.3	6.3	7.2	4.5	4.0	4.7	4.9	13.2	17.0	18.1	24.0	1.2	2.5	2.2	3.9	3.0	5.4	32688
211133_x_at	AF009643.1	sperm associated antigen 9	1.9	1.4	0.8	1.5	1.3	3.1	2.7	3.8	2.1	42.1	42.2	27.0	25.1	2.7	0.9	0.5	10.2	0.4	0.2	32526
219313_at	NM_017577.1	clone 6 immunoglobulin-like	0.0	0.8	0.2	0.0	0.4	0.2	0.1	0.1	0.0	3.8	3.7	3.1	5.6	0.2	0.1	0.1	0.0	1.2	0.1	32404
221149_at	NM_018485.1	transcript 5	0.2	0.1	0.8	0.7	1.2	0.7	0.9	0.9	0.6	3.3	3.2	4.2	2.9	0.0	0.3	0.2	1.0	0.1	0.3	32282
203433_at	NM_006441.1	G-protein-coupled receptor GRP77	1.4	1.8	1.5	2.5	1.6	3.1	4.2	3.5	3.1	15.8	11.4	9.6	9.0	1.6	1.8	1.9	2.9	1.7	1.5	32181
214486_x_at	AF041459.1	5, 10-methylenetetrahydrofolate synthetase	1.9	2.1	10.7	5.0	6.5	4.2	5.3	4.3	6.0	26.3	16.2	25.3	24.2	2.4	3.7	5.0	5.3	2.3	1.9	32114
		FADD-like apoptosis regulator																				

Fig. 61

28/36

C. Neutrophil (Ne)-selective transcripts (7/7).

Probe set		Accession #	Transcripts	MC cord blood	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pI	CD 4	CD 8	CD 14	CD 19	Fb	Ba S.I.
209222_s_at	202334_s_at	BC000296.1 AA877765	oxysterol binding protein-like 2 ubiquitin-conjugating enzyme E2B kinase 4	1.3 3.3	0.2 3.4	2.7 4.8	8.8 15.5	8.0 12.1	5.4 5.3	5.4 7.2	7.7 14.7	7.3 12.8	17.2 20.9	18.4 25.6	22.3 43.6	23.9 38.1	0.9 4.0	2.3 4.5	3.4 3.9	2.8 2.5	2.0 4.9	1.3 4.6	3.1877 3.1871
203266_s_at	58780_s_at	NM_003010.1 R42449	mitogen-activated protein kinase FLJ10357	3.7 4.5	2.4 5.4	4.9 1.5	8.2 3.9	6.3 3.0	2.5 7.8	4.8 9.6	6.8 12.8	5.0 16.4	14.7 28.0	15.2 27.6	27.4 46.7	26.9 44.1	2.8 1.2	2.4 0.6	2.6 0.1	2.7 6.5	2.3 0.2	2.7 5.7	3.1804 3.1803
210582_s_at	214766_s_at	AL117466.1 AL080144.1	LIM domain kinase 2 ELYS transcription factor-like protein TMB52	3.8 1.3	1.9 0.2	4.3 2.0	5.1 3.1	4.8 4.2	8.7 1.9	10.3 1.4	10.8 2.1	9.4 2.4	33.9 9.4	36.5 9.5	30.8 9.9	23.8 11.3	1.3 3.2	1.7 1.3	1.8 0.8	1.9 0.5	0.9 1.0	1.4 1.3	3.1609 3.1414
202266_at	203278_s_at	NM_016614.1 NM_016621.1	TRAF and TNF receptor-associated protein (AD022) BRAF35/HDAC2 complex (80 kDa) transmembrane gamma-carboxylglutamic acid protein 4	9.8 2.1	6.2 2.8	9.4 2.7	23.7 14.8	20.9 11.0	8.6 5.7	9.9 5.0	16.5 7.4	14.0 4.9	36.1 21.0	56.5 16.6	64.5 31.0	57.5 30.6	4.5 0.1	7.7 3.0	9.4 4.5	5.3 3.1	8.2 2.7	6.3 3.0	3.1402 3.1382
207291_at	213229_at	NM_024081.1 BE590131	ornithine decarboxylase antizyme clone 17.6 immunoglobulin-like transcript v-yes-1 Yamaguchi-sarcoma viral related oncogene homologue (LYN)	0.1 8.5	1.2 4.5	1.3 19.5	1.4 12.9	1.1 15.4	0.9 15.9	0.2 9.7	0.4 19.1	0.2 16.0	3.8 35.2	7.9 39.0	4.5 61.4	8.5 69.4	0.2 6.2	0.8 5.9	0.1 7.3	1.9 15.2	1.1 12.2	0.4 5.0	3.1336 3.1306
204204_at	201364_s_at	NM_001860.1 AF242521.1	solute carrier family 31 hypothetical protein MGC26706 major histocompatibility complex, class I B	1.7 8.3	1.7 7.3	1.3 4.4	0.3 2.2	0.8 1.9	1.7 11.5	0.9 21.9	2.3 8.0	1.2 7.7	22.6 61.9	23.8 59.1	31.3 21.0	36.0 27.7	2.0 2.2	1.2 5.1	1.2 6.3	8.9 12.2	0.2 6.2	0.4 9.6	3.1262 3.1253
210784_x_at	202625_at	AF009634.1 A3564412	v-yes-1 Yamaguchi-sarcoma viral related oncogene homologue (LYN) hypothetical protein MGC26706 major histocompatibility complex, class I B	1.4 6.9	0.1 5.0	2.1 5.4	1.2 5.2	2.4 5.8	2.5 5.2	2.2 3.4	2.8 7.6	2.1 5.1	52.1 14.8	48.8 12.0	31.8 77.5	36.3 19.2	0.8 2.0	0.2 2.4	0.2 2.1	0.2 5.2	0.3 7.5	0.2 1.6	3.1236 3.1131
37384_at		D13640	retinitis pigmentosa GTPase regulator interacting protein 1 (RGRIP1)	2.5 1.1	3.0 1.4	3.4 1.2	3.8 0.8	3.8 1.0	6.7 1.1	6.6 1.0	7.6 0.5	6.6 1.4	25.2 6.1	17.9 3.4	21.3 5.3	29.4 4.7	2.6 1.5	2.5 0.8	2.5 0.8	7.4 1.3	1.8 0.5	2.8 0.7	3.0985 3.091
206608_s_at	204924_at	NM_020366.1 NM_003264.1	Toll-like receptor 2 CD35, Fcγ APO-1	1.8 2.0	0.1 1.1	2.1 5.9	8.2 11.0	7.6 8.9	2.8 5.4	0.4 4.4	0.8 6.8	1.4 7.0	52.9 20.6	88.0 27.1	94.4 27.0	99.8 29.1	1.6 0.3	1.3 5.2	0.8 5.3	0.1 4.0	0.7 2.0	0.4 3.8	3.0909 3.0827
204781_s_at	212606_at	NM_000043.1 A806395	intercellular adhesion molecule 3 (ICAM3) carbonic anhydrase IV (CA4) metal phosphoesterase	2.0 3.1	2.0 2.9	0.0 20.1	0.7 19.4	0.6 31.9	0.7 11.6	0.0 11.9	0.1 20.6	0.1 19.1	18.0 58.8	14.3 74.1	25.0 72.8	26.9 81.0	0.1 4.1	0.2 6.8	0.3 8.7	6.6 10.3	0.0 5.5	3.4 2.6	3.0797 3.0752
211316_x_at	203045_at	AF009616.1 NM_004148.1	v-yes-1 Yamaguchi sarcoma viral related oncogene homologue (LYN) immunoglobulin superfamily, member 5 (GSF6)	4.4 3.0	2.5 3.7	3.2 5.7	6.4 46.3	4.8 34.5	10.7 38.9	9.7 51.6	18.5 94.5	12.1 93.7	29.3 161.1	34.1 168.3	44.7 239.1	46.1 241.1	0.5 4.5	1.2 13.6	1.7 21.0	8.3 17.6	0.2 19.9	2.9 1.3	3.0746 3.0617
204949_at	206208_at	NM_002162.2 NM_000717.2	zinc finger protein 267 v-rat-1 murine leukemia viral oncogene homologue 1 (RAF1)	0.2 2.1	0.6 1.7	0.1 5.0	0.1 15.0	0.1 12.1	1.1 8.9	0.7 13.7	1.0 25.4	0.8 23.9	5.6 49.9	5.2 28.3	2.8 59.9	2.4 75.8	1.2 0.7	0.1 4.5	0.1 6.6	0.1 5.7	0.1 5.4	0.1 3.7	3.0572 3.0554
213727_x_at	202626_s_at	A173554 NM_002350.1	mitogen-activated protein kinase kinase 4 IAR receptor-like protein-tyrosine phosphatase	15.5 1.1	9.5 0.3	12.1 0.2	12.7 0.4	14.8 0.7	32.6 1.9	31.6 1.2	54.0 1.1	41.0 1.0	110.1 17.5	115.1 24.2	122.7 30.6	172.2 33.3	18.4 1.4	2.1 0.4	1.5 0.4	36.8 8.4	33.0 0.3	0.6 0.3	3.0541 3.0442
206420_at	201651_s_at	NM_005849.1 NM_007229.1	kinase 4 zinc finger protein 267 v-rat-1 murine leukemia viral oncogene homologue 1 (RAF1)	21.4 2.0	17.4 1.0	4.6 1.3	24.8 3.7	20.1 3.6	13.3 2.0	19.5 1.5	33.9 4.4	35.3 3.7	61.3 6.7	72.5 6.9	76.1 9.2	94.4 9.9	24.7 1.0	4.9 2.1	4.4 1.3	8.6 1.0	6.1 1.6	8.0 0.1	3.0391 3.0361
219540_at	201244_s_at	AU150728 NM_002880.1	zinc finger protein 217 interferon-induced protein with tetrapeptide repeats 4 (IFIT4)	6.0 1.4	5.4 1.2	12.4 2.8	32.8 6.4	33.1 4.5	14.9 1.7	19.0 2.6	27.3 3.5	25.7 3.1	60.4 12.8	58.2 10.4	89.2 10.4	86.2 16.8	2.2 1.4	6.6 1.4	11.3 1.4	12.8 1.3	7.6 2.5	7.3 1.5	3.0329 3.028
203265_s_at	203030_s_at	AA810268 AF007555.1	IAR receptor-like protein-tyrosine phosphatase zinc finger protein 217	0.0 1.9	0.0 2.6	1.6 3.0	1.2 18.4	0.1 8.4	0.1 7.6	0.1 8.0	0.1 14.7	0.1 14.9	0.8 37.3	3.0 45.1	1.1 24.4	2.8 27.0	0.1 1.2	0.1 4.6	0.0 5.3	0.1 6.1	0.0 5.5	0.0 3.6	3.0269 3.0158
203739_at	204747_at	NM_006526.1 NM_001549.1	carbonic anhydrase IV (CA4) carbonic anhydrase IV (CA4)	2.0 0.7	3.0 1.0	4.9 0.8	6.0 0.6	3.5 0.6	4.3 2.2	12.4 2.1	4.4 1.5	3.0 2.1	24.2 13.8	27.0 7.4	15.4 4.7	12.0 3.5	0.3 2.1	1.8 1.0	1.2 0.5	6.2 0.9	1.4 1.0	2.6 0.5	3.0143 3.0112
206209_s_at		NM_000717.2	carbonic anhydrase IV (CA4)																				

Fig. 6J

D. Mast cell (MC)-selective transcripts (1/2).

Probe set	Accession #	Transcripts	MC cord	MC lung	Ba2	Ba3	EO	EO	EO3	EO4	Ne	Ne3	Ne4	p1	CD4	CD8	CD14	CD19	Fb	MCSL
217023_x_at	AF099143	tryptase beta	169.4	118.7	0.7	1.1	0.4	0.1	0.1	0.5	0.1	0.2	0.1	0.6	0.4	0.3	0.1	0.1	0.2	202.148
215382_x_at	AF206666.1	tryptase beta	168.1	108.4	1.7	0.7	0.4	0.2	0.2	0.2	0.1	0.1	0.3	0.1	0.1	0.7	0.1	0.1	0.1	172.668
204041_at	NM_000898.1	monoamine oxidase B	23.5	46.9	0.2	0.7	0.1	0.1	0.2	0.6	0.3	0.3	0.1	0.2	0.1	0.2	0.2	0.1	0.2	136.311
210084_x_at	AF206665.1	tryptase alpha	131.1	92.3	0.7	1.2	1.2	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.6	0.1	0.0	0.1	112.376
216474_x_at	AF206667.1	tryptase beta	210.0	120.9	2.4	2.0	1.4	1.2	0.4	0.2	0.1	0.2	1.1	0.1	0.1	1.8	0.8	0.9	0.1	84.3375
205683_x_at	NM_003294.2	tryptase beta	195.5	95.3	2.4	2.7	0.3	0.2	0.2	0.6	0.6	0.4	0.1	0.4	1.0	2.0	0.7	0.2	0.3	67.2617
207741_x_at	NM_003293.2	tryptase alpha	175.0	99.7	2.2	2.2	1.8	0.5	0.2	0.3	0.2	0.6	0.2	0.3	0.3	2.2	0.7	0.1	0.5	59.015
207134_x_at	NM_024164.2	tryptase beta	214.6	112.3	3.1	3.8	1.7	1.2	0.3	0.8	0.6	0.3	0.8	0.4	0.1	0.5	0.2	0.1	1.1	57.1834
205653_at	NM_001911.1	cathepsin G	91.2	57.0	2.7	1.1	0.9	0.9	0.4	3.1	0.8	0.3	1.4	1.6	0.6	0.7	0.2	0.4	1.3	51.4749
205266_at	NM_002309.2	leukemia inhibitory factor	17.0	9.8	0.2	0.2	0.3	0.3	0.1	0.2	0.2	0.1	0.2	0.4	0.7	0.1	0.2	0.1	0.1	44.3659
210324_at	M17263.1	complement protein C8 gamma	2.9	6.9	0.1	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.1	0.1	0.1	0.1	0.0	0.0	0.0	33.806
211743_s_at	BC005929.1	major basic protein	74.3	70.7	1.0	4.7	2.7	0.1	0.7	0.8	0.6	0.2	0.3	0.7	0.2	0.1	0.2	0.2	0.3	31.5959
211549_s_at	U63296.1	15-hydroxyprostaglandin dehydrogenase	48.3	48.3	2.1	2.5	1.4	1.5	1.3	0.8	0.9	0.1	0.1	0.2	0.1	1.1	0.5	0.8	0.5	24.8454
206726_at	NM_014485.1	prostaglandin D2 synthase	119.0	94.0	5.0	7.8	5.7	0.7	0.1	1.0	0.5	0.2	0.2	0.2	0.6	1.3	0.7	0.3	1.2	17.432
205011_at	NM_014622.1	loss of heterozygosity 11, chromosomal region 2, gene A	76.1	70.9	3.0	6.8	4.5	2.3	1.0	1.4	1.9	0.2	1.1	1.2	1.8	2.9	2.2	1.3	1.7	16.2511
205428_s_at	NM_001740.2	calbindin 2	16.7	63.4	1.3	0.7	0.9	0.4	1.6	0.7	1.3	1.8	1.6	3.6	1.5	1.7	0.7	1.1	1.3	16.1621
219255_at	NM_024554.1	FUJ1413	10.0	9.2	0.1	0.1	0.1	0.2	0.1	0.6	0.6	0.1	0.6	0.1	0.2	0.1	0.6	0.1	0.6	15.639
204468_s_at	NM_005424.1	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	3.6	2.8	0.5	0.3	0.1	0.0	0.1	0.2	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.1	14.4259
208343_s_at	AF146343.1	CYP7A promoter binding factor	1.5	0.9	0.0	0.0	0.3	0.1	0.0	0.1	0.0	0.1	0.0	0.2	0.4	0.1	0.0	0.0	0.0	13.8025
205051_s_at	NM_000222.1	CD117 c-Kit	92.1	85.8	6.2	8.1	7.3	2.3	5.2	6.5	2.7	0.7	2.1	0.8	1.1	0.8	0.2	0.5	0.1	12.3815
210102_at	BC001234.1	loss of heterozygosity 11, chromosomal region 2, gene A	40.9	41.1	2.8	3.7	4.5	0.3	0.4	0.3	0.6	0.7	0.9	0.2	0.6	1.8	0.8	0.7	1.2	11.3619
210796_x_at	D86359.1	siatic acid binding Ig-like lectin, siglec6	17.8	26.0	1.5	1.0	1.1	1.2	1.5	1.3	1.4	1.4	2.3	1.7	1.3	2.0	1.4	1.5	1.8	10.5398
206519_x_at	D86358.1	siatic acid binding Ig-like lectin, siglec6	3.4	7.9	0.0	0.3	0.4	0.0	0.0	0.0	0.1	0.0	0.1	0.5	0.2	0.5	0.0	0.0	0.0	10.13
206480_at	NM_000897.1	leukotriene C4 synthase	8.8	16.0	0.3	0.2	0.6	2.4	1.6	0.5	0.1	0.2	1.1	0.1	0.1	1.3	0.1	0.3	0.1	9.27381
206617_s_at	NM_002910.4	renin-binding protein	10.6	6.2	1.2	0.1	0.4	2.8	1.6	0.5	0.1	0.6	2.1	0.1	0.1	0.9	0.2	0.7	0.3	9.18529
208089_s_at	NM_030794.1	tudor domain containing 3	6.0	13.4	0.8	0.6	0.2	0.5	0.7	0.5	0.5	0.1	0.6	0.3	0.0	0.7	0.7	1.1	0.8	8.16897
205466_s_at	NM_005114.1	heparan sulfate 3-D-sulfotransferase ADAMTS3 a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3	18.1	7.2	0.1	0.4	0.1	0.7	0.1	0.3	0.2	0.4	0.1	0.8	0.4	0.1	0.0	0.0	0.2	8.15381
214913_at	AB002364.1	tissue-plasminogen activator	6.8	4.3	0.5	0.7	0.8	0.5	0.7	0.6	0.4	0.5	0.4	0.7	1.2	0.7	0.6	0.5	0.4	7.2214
201860_s_at	NM_000930.1	siatic acid binding Ig-like lectin, siglec6	22.2	29.7	0.2	0.4	0.1	0.1	0.3	0.5	0.5	0.1	0.1	1.3	0.4	1.6	0.1	0.2	0.6	7.10135
206520_x_at	NM_001245.1	LR8 protein	19.0	22.7	2.4	1.1	0.8	1.1	1.5	1.3	1.0	2.0	2.0	0.4	1.4	2.9	2.1	2.3	1.9	7.10132
220532_s_at	NM_014020.1	FLJ10305	52.4	18.2	0.8	0.8	1.0	6.4	2.9	1.5	1.2	0.4	0.3	1.4	0.6	2.2	0.6	0.2	5.0	6.1662
218165_at	NM_018052.1	nuclear receptor subfamily 1, group 1, member 3	6.2	14.6	0.3	0.2	0.4	0.4	0.3	0.3	0.4	0.6	0.5	0.1	0.1	0.5	0.2	1.4	1.6	6.04597
221728_x_at	AK025198.1	tudor domain containing 3	5.6	5.5	0.6	0.9	1.0	0.4	3.6	0.9	0.8	0.7	0.6	1.4	0.9	0.9	0.8	0.7	0.7	5.70228
214028_x_at	AU156998	lipase	3.2	11.9	0.9	0.0	0.4	0.8	0.3	0.4	0.7	0.6	0.6	0.1	0.1	0.8	1.2	1.1	0.1	5.10738
221552_at	BC001698.1	MKP-1 like protein tyrosine phosphatase (MKP-1)	10.6	3.4	0.9	1.8	1.1	0.9	1.1	1.0	0.9	0.2	0.2	0.7	0.1	0.1	0.2	0.7	0.9	5.02434
203367_at	NM_007026.1	heparan sulfate 6-O-sulfotransferase	15.0	45.4	1.2	0.9	0.8	0.9	0.9	0.8	0.1	0.2	0.7	0.4	2.0	0.9	1.0	2.7	0.5	5.00514
206997_s_at	NM_004807.1		4.2	3.8	0.2	0.1	0.1	0.4	0.4	0.1	0.3	0.3	0.4	0.3	0.7	0.3	0.2	0.6	0.3	4.81127

Fig. 6K

30/36

D. Mast cell (MC)-selective transcripts (2/2).

Probe set		Accession #	Transcripts	MC cord	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	EO 1	EO 2	EO3 (small)	EO4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MCSL
207480_s_at	45288_at	NM_020149.1 AA209239	TALE homeobox protein Meis2e lipase	140	149	19	36	40	17	19	53	38	03	06	10	03	05	08	04	06	04	08	472642
207039_at	201650_at	NM_000077.1 NM_002276.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) keratin 19	75	36	07	07	01	06	04	03	05	01	12	06	11	01	09	05	08	01	12	435629
214533_at		NM_001836.1	chymase	62	120	00	00	03	01	00	00	00	01	01	01	01	01	00	01	01	00	20	435547
				101	27	04	02	08	01	01	08	06	01	01	02	02	12	07	05	10	04	03	427984
218211_s_at	203916_at	NM_024101.1 NM_003635.1	melanophilin N-deacetylaseN-sulfotransferase	248	296	27	25	18	30	25	19	22	46	41	33	41	64	40	32	24	34	27	424499
			erythrocyte membrane protein band 4.1-like 1	179	267	32	65	68	25	27	36	31	42	34	55	52	09	31	49	33	27	24	420693
212336_at	200766_at	AB002336.1 NM_001909.1	cathepsin D	38	64	01	02	01	05	01	02	04	01	01	01	05	01	04	02	04	04	12	412758
202218_s_at	204066_s_at	NM_004265.1 NM_014914.1	delta-6 fatty acid desaturase (FADS6) centaurin, gamma 2	426	395	25	53	43	43	48	34	27	40	67	31	19	26	16	25	100	16	59	41037
				188	245	04	02	10	03	01	08	05	02	01	01	01	16	01	06	01	06	53	408548
				53	79	04	04	07	02	02	06	06	03	05	04	04	08	06	16	06	10	16	406712
209644_x_at	221679_s_at	U38945.1 AF725418.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) lipase	140	64	10	14	07	12	13	17	15	10	16	15	21	23	18	15	09	03	24	388459
211538_s_at	211548_s_at	U56725.1 J05594.1	heat shock protein 70kD 15-hydroxyprostaglandin dehydrogenase	28	19	04	09	01	03	04	04	01	01	05	00	05	05	01	06	06	05	02	383039
				44	74	03	06	04	06	03	03	09	14	04	10	08	15	05	05	01	05	07	380423
				826	600	194	260	163	32	29	18	17	08	05	09	02	41	12	09	01	06	02	349258
210174_at	219412_at	AF228413.1 NM_022337.1	member 2 RAB38, member RAS oncogene	29	34	05	05	06	08	11	07	12	11	04	01	04	09	07	02	02	06	03	347124
			gelosin-like capping protein (actin filament)	39	40	01	04	03	07	01	02	03	02	02	11	01	12	01	08	04	01	05	332805
201850_at	205888_s_at	NM_001747.1 A1962693	KIAA0555	705	645	96	308	288	81	78	115	99	26	36	30	24	16	11	10	170	58	53	329919
			3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	54	46	07	16	12	08	07	01	10	13	03	02	06	12	03	15	07	12	04	325197
221750_at		BG035985	nuclear receptor subfamily 1, group I, member 3	50	38	09	15	11	11	12	13	10	13	05	07	12	07	05	11	07	14	12	31926
214218_s_at	218788_s_at	AV699347 NM_022743.1	FLJ21080	35	35	07	06	07	05	22	05	05	07	12	06	01	11	09	03	06	08	04	315254
				161	237	05	23	25	09	11	27	21	11	10	08	09	23	21	29	06	20	63	307851
218087_s_at	221577_x_at	NM_015385.1 AF003934.1	SH3-domain protein 5 (ponsin) prostate differentiation factor	14	19	04	09	04	05	00	00	01	00	01	01	02	01	00	02	02	02	01	307366
	35820_at	X62078	GIM2 activator protein	78	55	06	03	05	06	01	02	06	00	02	03	01	01	02	00	01	04	21	305532
	208744_x_at	BG403660	heat shock 105kD	218	176	14	33	13	03	03	02	05	05	08	19	03	04	02	02	65	50	27	301647
				73	48	05	02	02	09	01	04	06	01	01	03	01	08	17	20	09	09	20	300671

Fig. 6L

31/36

E. Basophil and eosinophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC	MC	Ba 1	Ba 2	Ba 3	Eo	Eo	Eo 3	Eo 4	Ne	Ne	Ne 3	Ne 4	CD4	CD8	CD14	CD19	Fb	BasEoS
211517_s_at	M56651.1	<i>IL-5/interleukin 5 receptor alpha</i>	0.6	0.1	11.8	28.2	17.9	16.4	25.3	32.6	29.5	0.0	0.7	0.0	1.0	0.0	0.4	0.2	0.0	0.2	0.0
210744_s_at	M75914.1	<i>IL-5/interleukin 5 receptor alpha</i>	0.2	1.6	15.4	30.8	15.3	18.7	40.2	29.7	33.0	0.3	0.2	1.5	0.5	0.1	0.1	0.1	0.1	0.2	0.1
206361_at	NM_004778.1	<i>receptor-homologous molecule expressed on Th2 cells</i>	1.8	0.3	22.0	40.5	15.3	33.7	37.9	38.9	42.3	1.0	2.6	2.2	2.1	0.8	1.4	1.0	1.2	0.9	0.5
206207_at	NM_001828.3	<i>Charcot-Leyden crystal protein</i>	1.1	0.1	27.0	219.1	203.6	226.8	233.8	179.7	163.1	2.1	19.4	19.1	49.3	2.8	1.0	1.4	0.9	0.7	0.4
203638_s_at	NM_022566.1	<i>fibroblast growth factor R2</i>	0.2	0.1	7.3	43.5	33.0	4.1	8.8	12.3	23.3	0.1	0.1	0.3	0.3	0.1	0.1	0.2	0.1	0.1	1.0
207111_at	NM_001974.1	<i>egf-like module containing, much-like, hormone receptor-like sequence 1 (EMR-1)</i>	1.5	0.1	16.4	49.5	34.5	85.9	93.1	91.2	93.5	2.7	3.7	5.4	5.1	3.4	1.7	0.8	7.1	1.6	0.5
215248_at	AU14500.3	<i>FLJ1581 fts, clone HEMBA 1003598</i>	0.7	0.3	5.7	4.7	5.2	4.5	2.1	2.8	2.1	1.0	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.2
205471_s_at	AW772082	<i>dactylorhiza (Drosophila) homolog</i>	0.1	0.6	5.1	4.1	3.7	6.4	8.3	9.0	7.6	0.8	0.9	1.0	0.8	0.1	0.1	0.3	0.5	0.0	0.1
218857_s_at	NM_025080.1	<i>FLJ2316</i>	1.0	7.0	18.0	35.3	18.6	13.7	12.5	16.3	15.4	1.3	1.7	0.9	1.9	0.3	0.5	0.4	2.4	0.2	0.2
221169_s_at	NM_021624.1	<i>histamine receptor H4</i>	0.2	0.5	4.5	12.5	8.9	1.9	2.6	4.2	2.9	0.5	0.6	1.1	0.6	0.4	0.7	0.5	0.7	0.0	0.3
201769_at	NM_014666.1	<i>entrophin</i>	7.8	9.1	41.7	101.5	76.0	26.8	34.1	40.5	35.7	3.0	2.9	3.6	4.2	4.5	6.3	6.9	8.0	9.0	7.9
208228_s_at	M87771.1	<i>secreted fibroblast growth factor receptor (K-sam, Ilj)</i>	0.3	1.4	3.7	10.2	8.3	3.9	8.9	4.5	8.3	0.8	1.4	1.1	0.5	1.3	0.4	0.7	0.3	0.5	1.1
213605_s_at	AL049987.1	<i>hypothetical protein, MNCB-4779</i>	0.8	0.0	10.8	46.8	44.7	6.7	6.1	25.8	20.6	1.3	1.4	4.5	4.2	2.9	1.1	2.1	3.7	2.0	0.3
205382_s_at	NM_001928.1	<i>adipon</i>	3.5	0.1	62.0	206.0	176.5	62.4	48.1	60.5	44.8	7.1	32.5	20.5	16.3	0.1	0.6	0.1	15.6	0.1	3.8
49452_at	A057637	<i>hypothetical protein LOC283445</i>	0.6	0.2	5.2	7.7	6.6	6.9	5.9	10.2	12.7	1.1	0.2	0.3	1.3	0.1	1.6	1.6	0.5	1.3	0.8
220307_at	NM_016382.1	<i>CD244 natural killer cell receptor 2B4</i>	0.5	0.1	15.7	87.0	65.4	9.9	10.8	26.6	18.5	0.3	0.4	1.2	3.0	0.1	0.4	3.5	5.2	1.1	0.1
210108_at	BES0599	<i>calcium channel, voltage-dependent, L-type, alpha 1D subunit</i>	0.2	0.1	1.0	1.7	2.4	0.9	0.8	2.4	1.8	0.0	0.6	0.5	0.5	0.0	0.3	0.1	0.0	0.3	0.0
209193_at	M24779.1	<i>protein kinase-related oncogene (PIM1)</i>	6.8	7.1	61.3	110.3	100.1	47.0	79.7	91.6	79.5	19.2	18.8	21.1	16.1	4.1	12.7	13.9	4.6	4.0	1.2
202794_at	NM_002194.2	<i>inositol polyphosphate-1-phosphatase (INPP1)</i>	5.7	6.2	7.1	25.8	20.5	17.9	24.8	53.6	57.8	2.8	2.7	2.6	4.0	1.9	1.8	2.6	4.8	1.9	4.8
208304_at	NM_001857.1	<i>CCR3 chemokine (C-C motif) receptor 3</i>	0.2	1.1	107.2	142.9	102.2	46.4	91.7	118.1	107.5	28.3	20.0	26.3	25.1	0.2	0.5	0.4	0.2	0.2	0.4
206111_at	NM_002934.1	<i>eosinophil-derived neurotoxin</i>	2.2	2.0	33.7	71.4	38.4	104.7	80.8	47.7	45.1	2.0	2.3	3.1	2.8	1.4	0.7	0.4	14.8	0.7	0.5
43427_at	A0970898	<i>hypothetical protein LOC283445</i>	0.8	0.7	2.1	4.8	4.3	5.1	4.6	8.0	6.4	1.0	0.8	0.7	0.8	1.1	1.0	1.3	0.6	1.1	1.1
213804_at	A039084	<i>inositol</i>	0.6	1.2	4.3	8.0	6.8	8.6	5.6	6.3	9.7	0.7	0.5	2.2	1.7	1.4	1.2	1.4	1.0	1.9	1.3
208906_at	U62027.1	<i>polyphosphate-5-phosphatase, 75kD</i>	12.4	11.2	44.1	72.3	50.5	18.8	38.8	70.3	29.9	1.2	1.2	7.8	3.8	1.6	1.6	1.5	3.0	0.6	0.5
202804_at	A0539710	<i>Csr receptor</i>	8.5	7.0	24.2	56.2	48.9	14.2	20.0	30.1	20.7	3.0	3.6	4.3	6.0	3.8	3.5	5.4	5.1	5.5	5.3
221675_s_at	AF195624.1	<i>ATP-binding cassette, sub-family C (CFTR/MRP), member 1</i>	7.0	6.8	31.6	79.7	55.8	26.9	32.6	43.8	41.8	5.2	7.5	5.9	9.6	2.4	3.1	3.3	7.7	11.8	5.7
201562_s_at	NM_003104.1	<i>cholineresphosphotransferase 1 beta</i>	2.0	1.5	2.9	4.2	4.1	7.4	11.6	8.3	11.2	1.7	2.5	1.5	1.3	1.3	1.4	1.8	1.2	1.8	1.1
210230_at	BC003629.1	<i>sorbitol dehydrogenase (SORD)</i>	1.1	0.1	8.3	11.0	13.3	2.4	5.1	5.1	4.1	0.1	0.5	0.2	0.7	0.3	0.2	0.6	0.8	1.9	0.5
219919_s_at	NM_018276.1	<i>FLJ23438 fts, clone HIC13275</i>	0.1	0.2	3.1	1.8	2.5	1.7	4.3	1.7	2.1	0.1	0.5	0.4	0.3	0.1	0.1	0.1	0.1	0.1	0.7
204301_at	NM_014867.1	<i>KLAF0711</i>	0.6	0.1	3.8	14.3	10.7	5.3	6.8	12.6	10.5	1.2	0.6	1.6	1.6	1.0	0.8	1.2	2.6	0.8	0.1
210999_s_at	U66065.1	<i>Grb 10- and Grb-IR-related splice variant 1</i>	3.6	1.7	8.4	13.6	11.8	7.3	4.6	4.8	6.4	2.2	1.7	1.9	2.0	1.9	1.2	1.2	1.6	0.4	1.6
209539_at	D25304.1	<i>RacCdc42 guanine exchange factor (GEF) 6</i>	13.1	24.8	28.8	74.7	73.0	53.8	35.5	92.9	59.6	9.2	6.1	18.5	13.7	3.1	10.8	12.9	7.1	7.8	1.0
208921_s_at	L12387.1	<i>spicun (SR)</i>	19.2	11.4	20.2	88.6	67.0	37.4	42.4	86.3	85.4	6.9	8.9	17.6	21.5	2.6	11.1	12.7	8.4	8.6	17.8
209043_at	AF033026.1	<i>biomolecular ATP sulfonylaseadenosine 5-phosphosulfate kinase</i>	19.9	16.1	39.0	87.1	75.2	66.4	68.7	89.4	71.4	13.8	20.0	46.5	8.9	6.3	6.7	4.4	10.6	11.0	22.7

Fig. 6M

E. Eosinophil and neutrophil-selective transcripts (1/1).																						
MC		32/36																				
Probe set	Accession #	Transcripts	cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo1 (small)	Eo2 (small)	Eo3 (small)	Eo4 (small)	Ne1 (small)	Ne2 (small)	Ne3 (small)	Ne4 (small)	pl CD4	CD8	CD14	CD19	Fb	Eo+Ne+L	
212345_at	NM_005306.1	GPR43 PAR1-like zinc finger, DHHC domain containing 18	0.1	0.4	0.9	0.6	0.6	7.0	16.6	15.4	10.5	49.7	45.7	22.5	23.0	0.8	0.1	0.1	0.7	0.4	0.1	21.742
212860_at	BG168720	solute carrier family 19 member 1	2.2	0.8	4.1	3.9	4.0	16.0	17.4	14.8	16.7	59.2	53.9	30.9	39.8	1.1	2.4	3.8	2.6	1.5	1.3	6.5842
211576_s_at	BC003068.1	nephroblastoma overexpressed gene	1.4	0.1	0.7	1.4	0.7	5.1	5.9	11.5	12.4	19.8	18.7	27.1	28.1	1.8	0.9	0.4	2.7	0.5	0.8	4.99
214321_at	BF440025	ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3	1.3	1.0	0.8	0.2	0.7	6.2	7.2	17.0	13.7	4.5	7.6	10.7	11.3	0.1	0.1	0.0	0.1	0.1	1.8	4.9823
218950_at	NM_022481.1	BCL2-related protein A1	1.4	3.1	2.4	3.7	2.1	15.5	15.9	18.3	15.5	28.0	24.3	15.9	20.6	0.7	0.2	0.8	3.9	0.9	1.0	4.829
205681_at	NM_004049.1	granulysin	0.5	1.9	1.0	3.2	2.4	52.4	40.2	35.9	30.5	46.5	49.2	35.5	33.5	1.5	2.2	1.9	8.3	4.3	0.2	4.7782
203765_at	NM_012198.1	cDNA FLJ36416 fs, clone	2.0	1.8	4.5	11.7	8.3	27.5	39.8	46.7	34.8	71.6	85.2	80.5	77.9	1.0	1.0	1.2	12.1	3.1	0.5	4.4403
213241_at	AF035307.1	THYMU2011053	5.0	2.4	1.6	1.0	1.0	33.2	37.1	68.7	40.6	63.2	77.8	89.2	80.9	3.0	3.0	2.8	13.5	4.1	7.8	4.2603
221815_at	BE671816	hypothetical protein PRO2831 homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	1.2	1.4	1.3	0.5	1.6	10.1	8.8	11.2	6.4	5.0	6.2	4.0	3.8	1.6	0.8	0.2	1.4	0.9	0.6	4.1325
214153_at	BE467941	KIAA0599	1.0	0.6	1.0	2.0	3.1	9.1	10.4	18.2	16.6	9.7	9.7	14.5	15.2	0.8	0.9	1.2	0.7	2.3	0.1	4.0797
212821_at	AU147160	Edg4, endothelial differentiation lysophosphatidic acid	0.1	0.1	0.4	1.2	0.9	4.6	2.8	4.7	3.4	4.4	3.5	6.0	7.9	0.4	0.2	0.4	0.3	0.0	0.2	3.777
206723_s_at	AF011466.1	G-protein-coupled receptor, 4 adenosine monophosphate deaminase 2 (isoform L)	1.2	1.4	2.1	3.6	2.6	13.7	8.0	19.6	22.3	24.6	17.0	26.1	29.1	0.1	3.6	5.0	3.8	1.9	0.9	3.7119
212360_at	A1916249	transforming, acidic coiled-coil containing protein 3 (TACC3)	1.0	2.0	2.6	5.9	4.6	26.6	18.7	30.2	31.9	78.7	63.1	79.5	91.3	3.4	5.8	6.1	12.6	3.7	5.8	3.5888
218308_at	NM_006342.1	protein kinase C-like 2	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769
212629_s_at	AK023692.1	serum glucocorticoid regulated kinase (SGK)	1.9	0.6	3.1	3.7	5.1	11.8	7.6	17.7	13.8	16.7	23.6	27.0	28.4	1.1	2.1	2.2	4.2	4.2	2.9	3.2963
201739_at	NM_005627.1	ectonucleoside triphosphate diphosphohydrolase 1	30.2	25.2	1.9	18.5	25.4	114.1	116.0	150.9	164.8	60.2	77.1	105.8	156.3	1.1	3.7	0.7	34.6	1.6	18.9	3.2456
209473_at	AV717590	growth arrest and DNA damage inducible protein beta (GADD45B)	1.4	0.6	2.1	1.6	2.0	15.9	22.3	39.5	29.1	14.1	13.7	23.7	13.8	2.6	2.6	1.3	6.5	4.8	0.6	3.0752
209304_x_at	AF087853.1	iduronate 2-sulfatase	2.0	0.3	2.7	4.5	3.6	15.5	11.9	16.3	34.4	7.0	12.0	13.5	9.4	0.4	3.1	4.2	4.1	3.7	0.6	3.0295
210666_at	AF050145.1		0.1	0.3	1.3	0.5	1.7	7.1	2.9	3.3	3.8	6.1	5.1	5.2	10.8	0.4	0.1	0.9	0.7	0.4	0.1	3.0005

Fig. 6N

G. Basophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	cord blood	MC	Ba1		Ba2		Ba3		Eo		Eo4		Ne		Ne3		Ne4		CD4	CD8	CD14	CD19	Fb	Ba+Ne.S.L.
					lung	small	small	small	1	2	small	small	1	2	small	small	pl									
218739_at	NM_016006.1	CGI-58 protein	1.8	1.8	7.2	16.3	17.3	2.6	3.3	3.2	2.5	20.7	23.6	21.4	19.3	1.3	1.2	0.7	2.9	0.7	1.5	5.81398				
219242_at	NM_025180.1	FLJ13386	1.0	0.3	10.1	23.5	18.8	24	3.7	4.5	4.2	13.7	14.0	26.1	27.7	0.1	0.5	1.6	1.0	0.6	2.5	4.97025				
219157_at	NM_007246.1	kelch (Drosophila)-like 2	2.4	1.7	4.2	16.2	19.2	3.6	2.5	4.3	3.8	15.5	24.4	24.5	22.5	0.7	2.0	1.5	3.0	2.2	1.7	4.61523				
206643_at	NM_002108.2	histidine ammonia-lyase	0.1	1.4	8.5	13.7	25.4	0.2	0.6	1.3	0.6	31.4	32.8	61.7	37.0	1.6	0.5	0.1	5.6	0.6	0.5	4.57355				
213935_at	AF007132.1	clone 23551 mRNA	0.8	0.1	5.0	26.2	26.4	2.4	1.7	2.9	1.2	4.5	6.7	11.2	9.0	0.1	0.1	0.2	2.3	0.5	0.8	4.33664				
222151_s_at	AK023738.1	FLJ13676 fs	1.0	0.9	4.5	5.5	4.7	1.8	1.7	1.4	1.6	8.4	10.2	8.4	7.6	0.5	0.8	1.3	0.8	1.0	1.3	4.14372				
207907_at	NM_003807.1	tumor necrosis factor (ligand)	0.1	0.1	3.9	10.4	6.3	1.2	1.5	4.0	4.1	15.8	7.3	15.8	11.5	0.2	0.4	0.1	0.6	0.0	0.1	3.89177				
202530_at	NM_001315.1	superfamily member 14 (TNF-SF 14)	5.0	3.0	28.8	82.2	70.8	4.0	7.1	13.9	11.1	13.6	23.0	25.7	22.3	5.3	2.9	3.5	7.3	2.6	4.5	3.8469				
217521_at	N54942	mitogen-activated protein kinase 14	0.1	0.1	5.5	18.9	20.9	0.3	0.3	1.6	0.1	19.6	14.5	29.9	18.4	0.4	0.8	0.9	4.3	1.0	0.3	3.84207				
203693_s_at	NM_001949.2	Hs276590 ESTs	2.5	1.7	4.3	16.2	13.2	2.1	1.9	5.7	3.3	8.8	11.7	13.3	15.4	1.5	1.4	2.5	2.3	1.1	1.2	3.7116				
203420_at	NM_016255.1	E2F transcription factor 3	2.4	3.3	15.6	31.5	32.4	7.3	6.6	14.3	11.0	37.2	37.2	48.5	50.0	6.1	5.0	9.8	4.5	3.3	9.8	3.48188				
218308_at	NM_006342.1	autosomal highly conserved protein (AHCP)	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769				
203080_s_at	NM_013450.1	transforming acidic coiled-coil containing protein 3	2.2	2.4	10.4	22.8	22.9	4.9	6.6	10.0	9.5	29.5	30.7	33.5	40.6	1.1	1.7	1.9	4.6	2.3	1.5	3.401				
219999_at	NM_018621.1	bromodomain adjacent to zinc finger domain, 2B	0.4	0.6	3.9	7.6	8.0	2.0	1.5	3.9	2.7	9.8	6.5	11.7	12.3	0.2	1.3	1.8	2.4	1.7	0.9	3.31991				
213805_at	AI692428	hypothetical protein PRO2198	0.3	0.1	13.8	11.0	8.7	3.2	3.0	1.4	1.4	19.7	16.7	5.3	7.0	0.7	0.2	0.8	3.3	0.4	0.7	3.29317				
204669_s_at	NM_007219.2	clone 23551 mRNA	0.9	0.2	4.4	27.9	34.3	2.1	5.9	16.1	14.5	18.8	14.4	60.7	56.1	0.5	0.1	0.1	0.1	0.1	0.8	3.18834				
215555_at	AK023774.1	ring finger protein 24	0.0	0.4	5.0	4.3	5.8	1.5	1.9	1.5	1.5	7.6	8.2	3.3	3.2	0.9	1.0	1.5	1.5	1.0	0.1	3.1591				
		FLJ13712 fs																								

33/36

Fig. 60

34/36

H. Mast cell and basophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pI	CD 4	CD 8	CD 14	CD 19	Fb	MC+Ba SL
205624_at	NM_001870.1	Carboxypeptidase A3	137.1	91.0	107.6	139.0	173.1	2.5	1.6	2.8	1.9	0.1	1.4	2.0	12.4	0.2	1.2	0.2	0.2	0.5	0.5	591989
208605_s_at	NM_002529.2	R TRK neurotrophin receptor regulator of G protein signaling (RGS13)	8.0	1.2	4.6	9.3	8.1	0.2	0.2	0.0	0.1	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	34.7309
210258_at	AF030107.1	Fc epsilon RI beta	62	8.4	5.6	7.1	10.9	0.3	0.1	0.4	0.5	0.5	0.0	0.1	0.3	0.1	0.0	0.0	0.2	0.3	0.0	21.7762
207496_at	NM_000139.1	R solute carrier family 18	199	24.7	35.4	51.9	45.6	0.9	0.1	0.5	0.3	0.1	0.1	0.5	1.8	1.6	0.5	0.2	0.0	0.3	0.1	21.1783
205857_at	AI269290	GATA-binding protein 2	24.3	27.1	8.1	22.3	25.0	1.3	1.0	0.8	0.9	1.3	0.9	0.5	0.7	0.9	0.4	0.3	0.2	0.3	0.3	20.3301
210358_x_at	BC002557.1	Fc epsilon RI beta	18.4	12.8	55.0	31.7	24.7	2.0	1.6	1.9	1.7	0.9	1.9	1.3	3.7	2.6	0.8	0.8	0.9	0.4	2.7	9.46893
207497_s_at	D10583.1	15-hydroxyprostaglandin dehydrogenase (PDGH)	10.7	28.6	34.9	12.6	6.8	1.5	1.0	0.8	0.8	1.9	0.9	1.7	1.5	1.7	0.7	0.7	0.1	0.3	0.5	9.39967
203914_x_at	NM_000860.1	chromosome 11 open reading frame 14	63.9	51.4	24.8	36.0	23.3	4.1	4.6	4.6	2.6	1.3	0.9	1.3	1.2	6.0	1.4	1.5	0.4	0.8	0.4	6.14285
219557_s_at	NM_020645.1	protein kinase, X-linked	7.4	4.2	4.4	7.4	6.6	1.2	1.6	2.0	2.4	0.9	1.9	1.1	2.1	1.1	1.4	1.4	1.5	0.4	1.6	3.38029
204061_at	NM_005044.1	low density lipoprotein receptor	6.2	5.2	5.2	12.8	16.9	2.3	2.7	2.5	2.4	0.8	0.4	0.7	1.2	1.9	1.5	2.1	2.5	2.0	0.8	3.26062
202068_s_at	NM_000527.2	R	24.6	16.8	19.3	28.5	13.5	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	2.3	2.1	3.4	3.5	0.8	6.3	3.1679

Fig. 6P

35/36

I. Specific transcripts markers for non-granulocytes.

Probe set	Accession #	Transcripts	MC		Ba 1	Ba 2	Ba 3	Eo 1	Eo 2	Eo 3	Eo 4	Ne 1	Ne 2	Ne 3	Ne 4	pl	CD4	CD8	CD14	CD19	Fb
			cord	blood	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)
203547_at	U47924	CD4	5.5	4.7	2.2	1.1	1.2	2.0	1.6	0.4	0.9	0.7	1.1	0.7	0.8	3.5	15.0	0.3	17.6	1.2	0.4
205758_at	AW006735	CD8	0.5	1.7	2.6	2.3	3.2	1.3	1.1	2.2	1.7	0.3	0.5	1.8	0.3	4.2	3.0	76.1	0.8	0.6	0.4
206398_s_at	NM_001770.1	CD19	0.7	0.1	0.7	0.4	0.7	0.8	0.5	0.5	0.2	0.6	1.5	1.1	0.7	4.0	0.0	0.1	0.1	19.1	0.4
211644_x_at	L14458.1	IgGVJ-region	0.2	0.1	0.1	0.1	0.2	0.2	0.2	0.2	0.3	0.1	0.3	0.2	0.2	3.8	0.1	0.2	0.1	70.9	0.1
201743_at	NM_000591.1	CD74	18.4	2.4	0.3	0.1	0.6	8.8	0.6	1.1	3.2	40.7	49.6	58.7	68.2	2.9	0.4	0.0	97.2	1.1	0.9
203104_at	NM_005211.1	v-fms-M-CSF receptor	3.8	0.2	0.6	0.7	0.3	3.0	1.1	1.7	1.5	8.8	8.7	6.3	6.4	5.2	2.8	0.7	42.1	1.4	0.9
209968_s_at	U63041.1	CD56	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.2	0.1	0.0
204627_s_at	M35999.1	CD61 glycoprotein IIIa	1.7	9.4	0.2	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.4	0.1	0.2	48.3	0.1	0.3	0.1	0.2	0.5
216442_x_at	AK026737.1	fibronectin	0.3	1.5	0.3	0.3	0.2	0.1	1.0	0.3	0.6	0.1	0.1	0.2	0.1	0.3	0.1	1.0	0.3	0.1	92.6

Fig. 6Q

J. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes.

Probe set	Accession #	Transcripts	MC		Ba 2		Ba 3		Eo		Eo 3		Eo 4		Ne		Ne 3		Ne 4		pI	CD4	CD8	CD14	CD19	Fb
			cord	lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)											
AFFX-HSAC07/X00351_3_at	X00351	beta-actin	18534	19383	14638	20922	19151	22019	18638	21153	18568	19406	22302	16589	17569	18295	18782	20805	20661	17542	20399					
AFFX-HSAC07/X00351_M_at	X00351	beta-actin	22898	21777	12940	11533	7608	22560	18785	14861	13431	23106	23373	6861	8019	19368	20362	22761	22294	19087	22757					
AFFX-HSAC07/X00351_5_at	X00351	beta-actin	15642	15838	9516	2927	2066	17186	21061	4861	3771	18772	19768	2165	2193	14887	16381	18218	17583	15063	16795					
AFFX-HUMGAPDH/M33197_3_at	M33197	GAPDH	14906	13632	3640	10477	9332	2649	2844	5498	2605	2549	3186	3586	3538	5929	6429	6098	9756	5180	19674					
AFFX-HUMGAPDH/M33197_M_at	M33197	GAPDH	15891	16852	3218	7587	6963	2382	2565	3720	1838	2194	2796	2312	2154	6182	5931	5971	11464	4344	17013					
AFFX-HUMGAPDH/M33197_5_at	M33197	GAPDH	16298	16701	3479	4559	5110	1827	3121	2127	1168	2492	3476	1636	1355	4655	6826	6260	9905	5636	23350					
The median value of 2283 transcripts			121	1693	853	1122	1109	93.7	102.1	127.3	114	62.7	73.1	87.4	87.3	82.3	152.5	121.3	107.1	114.1	183.8					

Abbreviations used in the table A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

Fig. 6R

36/36